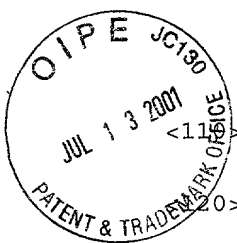


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<110> Burgess, Catherine E.

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ttg ctg ggg aaa gca ctc cag gtg ggt gtt act aca aat cac cgt ctg 96

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ctg acc cac tgg tac tac ctg aca gcc ttt gat att tcc aga gtc aat 144

Leu Thr His Trp Tyr Tyr Leu Thr Ala Phe Asp Ile Ser Arg Val Asn

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acc tgc ttt cca ttc tcc aca gca tct aat ata agt cat ggc ttc tca 192

Thr Cys Phe Pro Phe Ser Thr Ala Ser Asn Ile Ser His Gly Phe Ser

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tct gtc ctg ctt ccc cgc ttc gcg ttc acc act gtg ctg aga tat agg 240

Ser Val Leu Leu Pro Arg Phe Ala Phe Thr Thr Val Leu Arg Tyr Arg

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 Glu Arg Asn Gly Asn Lys Glu Ala Ile Ala Gly Leu Ser Ser Ser Gly
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ggc ttc aca gct tgc ctc ctc ctt cgt ctg ttg agt cat ccc aca cgc 336
 Gly Phe Thr Ala Cys Leu Leu Leu Arg Leu Leu Ser His Pro Thr Arg
 100 105 110

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Leu Thr His Trp Tyr Tyr Leu Thr Ala Phe Asp Ile Ser Arg Val Asn
 35 40 45

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Ser Val Leu Leu Pro Arg Phe Ala Phe Thr Thr Val Leu Arg Tyr Arg
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Glu Arg Asn Gly Asn Lys Glu Ala Ile Ala Gly Leu Ser Ser Ser Gly
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Lys Leu Val Ser Ser Glu Arg Ala Ser Gly Glu Ala Leu Lys Leu His
35 40 45

aac tat aga gtc ctc agc tgc aca agc ccc ctg ctg ttc cag ctc caa 192
Asn Tyr Arg Val Leu Ser Cys Thr Ser Pro Leu Leu Phe Gln Leu Gln
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Pro Leu Leu Asp Tyr Asn His Met Ile Leu Ser Asn Leu Ala Pro Asp
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gtc agg gtg cca ctg agt atg cag tat gct gac tta atc ata aaa att 288
Val Arg Val Pro Leu Ser Met Gln Tyr Ala Asp Leu Ile Ile Lys Ile
85 90 95

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Asn Thr Phe Ser Ile Gln Ala Ala His Ile Thr His Lys Phe Leu Phe
100 105 110

aac aaa gaa agg cat gca ttt cat aca cgg gga caa ttc ggt cag att 384
Asn Lys Glu Arg His Ala Phe His Thr Arg Gly Gln Phe Gly Gln Ile
115 120 125

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Val Ser Ser Gln Tyr Leu Tyr Glu Ile Asn Cys Thr Glu Gly Met Pro
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Gly Ser Phe Arg Gly Gly Glu Val Arg Gly Ser Gly Thr Arg Leu Gly

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Pro Leu Leu Asp Tyr Asn His Met Ile Leu Ser Asn Leu Ala Pro Asp
 65 70 75 80

Val Arg Val Pro Leu Ser Met Gln Tyr Ala Asp Leu Ile Ile Lys Ile
 85 90 95

Asn Thr Phe Ser Ile Gln Ala Ala His Ile Thr His Lys Phe Leu Phe
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Asn Lys Glu Arg His Ala Phe His Thr Arg Gly Gln Phe Gly Gln Ile
 115 120 125

Val Ser Ser Gln Tyr Leu Tyr Glu Ile Asn Cys Thr Glu Gly Met Pro
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Ile Phe Thr Arg Arg Thr Lys Val Glu Val Asn Asn Phe Glu Ala Trp
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 Pro Pro Leu Phe Ser Gln Cys Gly Gly Ser Gly Cys Ser Arg Gln Pro
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 Thr Ile Pro Ile Ser Asn Met Glu Gly Gln Ile Cys Val Lys Pro Ser
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 Gly Ala Lys Ala Ala Pro Glu Pro Leu Glu Glu Leu Ser Lys Met Arg
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 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
 65 70 75 80

cct gca atc aaa cat gct aaa gca gag aaa tac aat aag aga cct ata 288
 Pro Ala Ile Lys His Ala Lys Ala Glu Lys Tyr Asn Lys Arg Pro Ile
 85 90 95

ctt gac att agc aga gga agt cca gct gtg tac act aat tat gat aaa 336
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 His Pro Phe Thr Met Ser Gly Arg Arg Leu Ala Thr Asp Leu Glu Arg
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 Ser Leu Ser Ser Ile Pro Trp Tyr Ile Leu Ser Phe Ser Ser Ala Glu
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 Leu Asp Ile Ser Arg Gly Ser Pro Ala Val Tyr Thr Asn Tyr Asp Lys
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Arg Arg Arg Val Phe Gly Leu Leu Glu Arg Pro Val Leu Leu Pro Pro	
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Val Ser Ile Asp Thr Ala Ser Tyr Lys Ile Phe Val Ser Gly Lys Ser	
50 55 60	
ggg gtg ggc aag acg gcg ctg gtg gcc aag ctg gct ggc ctg gag gtg	240
Gly Val Gly Lys Thr Ala Leu Val Ala Lys Leu Ala Gly Leu Glu Val	
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Pro Val Val His His Glu Thr Thr Gly Ile Gln Thr Thr Val Val Phe	
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Trp Pro Ala Lys Leu Gln Ala Ser Ser Arg Val Val Met Phe Arg Phe	
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Glu Phe Trp Asp Cys Gly Glu Ser Ala Leu Lys Lys Phe Asp His Met	
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Phe Thr Asp Arg Ala Ser Phe Glu Asp Leu Pro Gly Gln Leu Ala Arg	
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Phe Arg Gln Ala Trp Glu Leu Pro Leu Leu Arg Val Lys Ser Val Pro	
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210 215 220	
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260 265 270	
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Leu Arg Gln Arg Arg Trp Arg Glu Asn Phe Gln Arg Asn Leu Glu Glu	
325 330 335	
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385 390 395 400	

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420 425 430	
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Ala Pro His His Trp Asp Cys Ser Asp Phe Gln Asp Gln Glu Val Met	
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Cys Leu Ser His Leu Leu Thr Ser Ser Ala Ala Ile Leu Thr Val Leu	
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Cys Val Val Met Ile Phe Leu Val Ser Val Ile Ile Tyr His Gly Ile	
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Ile Ser Ile Ala Met Phe His Thr Gly Asn Ser Val Leu Met Thr Gln	
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Leu Cys Val Cys Gln Gln Gln Cys Gly Pro Gly Gly Cys His Ile Gln	
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625 630 635 640	
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Ile Gly Leu Asp Ala His Lys Phe Leu Cys Lys Tyr Gln Arg Pro Met	
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Cys Glu Leu Ile Leu Pro Arg Thr Asn Ala Arg Ser Arg Leu Gly Tyr	
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725 730 735	
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Gln Leu Gly Arg Glu Arg Ala Ser Pro Ala Gly Thr Ala Lys Gln His	
770 775 780	

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Arg Gly Met Asp Cys Gly Pro Pro Ala Thr Leu Gln Pro His Leu Thr	
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Gly Pro Pro Gly Thr Ala His His Pro Val Ala Val Cys Gln Gln Glu	
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835 840 845	
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Cys Leu Asp Leu Phe Pro Val Ala Pro Glu Glu Leu Arg Ala Pro Gly	
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865 870 875 880	
cca tta tcc cca gga ggc tca gat aca gag atc acc agc ggg ggg atg	2688
Pro Leu Ser Pro Gly Gly Ser Asp Thr Glu Ile Thr Ser Gly Gly Met	
885 890 895	
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Arg Pro Ser Arg Ala Gly Ser Trp Pro His Cys Pro Gly Ala Gln Pro	
900 905 910	
cca gct ctg gag gga ccc tgg agt ccc cga cac aca cag cca cag cgc	2784
Pro Ala Leu Glu Gly Pro Trp Ser Pro Arg His Thr Gln Pro Gln Arg	
915 920 925	
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Arg Ala Ser His Gly Ser Glu Lys Lys Ser Ala Trp Arg Lys Met Arg	
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Val Tyr Gln Arg Glu Glu Val Pro Gly Cys Pro Glu Ala His Ala Val	
945 950 955 960	
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Phe Leu Glu Pro Gly Gln Val Val Gln Glu Gln Ala Leu Ser Thr Glu	
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Glu Pro Arg Val Glu Leu Ser Gly Ser Thr Arg Val Ser Leu Glu Gly	
980 985 990	
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Pro Glu Arg Arg Arg Phe Ser Ala Ser Glu Leu Met Thr Arg Leu His	
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Ser Ser Leu Arg Leu Gly Arg Asn Ser Ala Ala Arg Ala Leu Ile Ser	
1010 1015 1020	
ggg tca ggc acc gga gca gcc cgg gaa ggg aaa gca tct gga atg gag	3120
Gly Ser Gly Thr Gly Ala Ala Arg Glu Gly Lys Ala Ser Gly Met Glu	
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Asp Glu Ala Glu Gly Ala Glu Glu Gly Pro Gly Pro Pro Arg Ala Asn	
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Thr Phe Ser Leu Trp Gln Asp Ile Pro Asp Val Arg Gly Ser Gly Val	
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Leu Ala Thr Leu Ser Leu Arg Asp Cys Lys Leu Gln Glu Ala Lys Phe	
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Ser Glu Arg Phe Leu Gln Asp Leu Glu Gln Arg Leu Glu Ala Asp Val	
1235 1240 1245	
 ctg cgc ttc agc gtg tgc gac gtg gtg ctg gac cac tgc ccg gcc ttc	3792
Leu Arg Phe Ser Val Cys Asp Val Val Leu Asp His Cys Pro Ala Phe	
1250 1255 1260	
 cgc aga gtc tac ctg ccc tat gtc acc aac cag gcc tac cag gag cgc	3840
Arg Arg Val Tyr Leu Pro Tyr Val Thr Asn Gln Ala Tyr Gln Glu Arg	
1265 1270 1275 1280	
 acc tac cag cgc ctg ctc ctg gag aac ccc agg ttc cct ggc atc ctg	3888
Thr Tyr Gln Arg Leu Leu Leu Glu Asn Pro Arg Phe Pro Gly Ile Leu	
1285 1290 1295	
 gct cgc ctg gag gag tct cct gtg tgc cag cgt ctg ccc ctt acc tcc	3936
Ala Arg Leu Glu Glu Ser Pro Val Cys Gln Arg Leu Pro Leu Thr Ser	
1300 1305 1310	
 ttc ctt atc ctg ccc ttc cag agg atc acc cgc ctc aag atg ttg gtg	3984
Phe Leu Ile Leu Pro Phe Gln Arg Ile Thr Arg Leu Lys Met Leu Val	
1315 1320 1325	
 gag aac atc ctg aag cgg aca gca cag ggc tct gaa gac gaa gac atg	4032
Glu Asn Ile Leu Lys Arg Thr Ala Gln Gly Ser Glu Asp Glu Asp Met	
1330 1335 1340	
 gcc acc aag gcc ttc aat gcg ctc aag gag ctg gtg cag gag tgc aat	4080
Ala Thr Lys Ala Phe Asn Ala Leu Lys Glu Leu Val Gln Glu Cys Asn	
1345 1350 1355 1360	

gct agt gta cag tcc atg aag agg aca gag gaa ctc atc cac ctg agc	4128
Ala Ser Val Gln Ser Met Lys Arg Thr Glu Glu Leu Ile His Leu Ser	
1365 1370 1375	
aag aag atc cac ttt gag ggc aag att ttc ccg ctg atc tct cag gcc	4176
Lys Lys Ile His Phe Glu Gly Lys Ile Phe Pro Leu Ile Ser Gln Ala	
1380 1385 1390	
cgc tgg ctg gtt cgg cat gga gag ttg gta gag ctg gca cca ctg cct	4224
Arg Trp Leu Val Arg His Gly Glu Leu Val Glu Leu Ala Pro Leu Pro	
1395 1400 1405	
gca gca ccc cct gcc aag ctg aag ctg tcc agc aag gca gtc tac ctc	4272
Ala Ala Pro Pro Ala Lys Leu Lys Leu Ser Ser Lys Ala Val Tyr Leu	
1410 1415 1420	
cac ctc ttc aat gac tgc ttg ctg ctc tct cgg cgg aag gag cta ggg	4320
His Leu Phe Asn Asp Cys Leu Leu Leu Ser Arg Arg Lys Glu Leu Gly	
1425 1430 1435 1440	
aag ttt gcc gtt ttc gtc cat gcc aag atg gct gag ctg cag gtg cgg	4368
Lys Phe Ala Val Phe Val His Ala Lys Met Ala Glu Leu Gln Val Arg	
1445 1450 1455	
gac ctg agc ctg aag ctg cag ggc atc ccc ggc cac gtg ttc ctc ctc	4416
Asp Leu Ser Leu Lys Leu Gln Gly Ile Pro Gly His Val Phe Leu Leu	
1460 1465 1470	
cag ctc ctc cac ggg cag cac atg aag cac cag ttc ctg ctg cgg gcc	4464
Gln Leu Leu His Gly Gln His Met Lys His Gln Phe Leu Leu Arg Ala	
1475 1480 1485	
cgg acg gaa agt gag aag cag cga tgg atc tca gcc ttg tgc ccc tcc	4512
Arg Thr Glu Ser Glu Lys Gln Arg Trp Ile Ser Ala Leu Cys Pro Ser	
1490 1495 1500	
agc ccc cag gag gac aag gag gtc atc agt gag ggg gaa gat tgc ccc	4560
Ser Pro Gln Glu Asp Lys Glu Val Ile Ser Glu Gly Glu Asp Cys Pro	
1505 1510 1515 1520	
cag gtt cag tgt gtt agg aca tac aag gca ctg cac cca gat gag ctg	4608
Gln Val Gln Cys Val Arg Thr Tyr Lys Ala Leu His Pro Asp Glu Leu	
1525 1530 1535	
acc ttg gag aag act gac atc ctg tca gtg agg acc tgg acc agt gac	4656
Thr Leu Glu Lys Thr Asp Ile Leu Ser Val Arg Thr Trp Thr Ser Asp	
1540 1545 1550	

130		135		140
Phe Thr Asp Arg Ala Ser	Phe Glu Asp Leu Pro Gly Gln Leu Ala Arg			
145	150	155		160
Ile Ala Gly Glu Ala Pro Gly Val Val Arg Met Val Ile Gly Ser Lys				
	165	170		175
Phe Asp Gln Tyr Met His Thr Asp Val Pro Glu Arg Asp Leu Thr Ala				
	180	185		190
Phe Arg Gln Ala Trp Glu Leu Pro Leu Leu Arg Val Lys Ser Val Pro				
	195	200		205
Gly Arg Arg Leu Ala Asp Gly Arg Thr Leu Asp Gly Arg Ala Gly Leu				
	210	215		220
Ala Asp Val Ala His Ile Leu Asn Gly Leu Ala Glu Gln Leu Trp His				
	225	230		235
Gln Asp Gln Thr Ala Met Thr Pro Pro Thr Gly Arg Arg Leu Cys Leu				
	245	250		255
Ala Pro Cys Gly Gly Ile Tyr Val Pro Asp Ser Arg Gly Thr Phe Ser				
	260	265		270
Glu Thr Gly Lys Pro Ala Leu Ile Lys Val Gly Gln Ser Gly Val Arg				
	275	280		285
Pro Leu Leu Thr Val Pro Leu Thr Pro Arg Trp Val Arg Leu Arg Ala				
	290	295		300
Arg Leu Gly Gly Glu Ala Ala Thr Pro Ala Ala Ala Gly Glu Arg Arg				
	305	310		315
Leu Arg Gln Arg Arg Trp Arg Glu Asn Phe Gln Arg Asn Leu Glu Glu				
	325	330		335
Gly Leu Phe Glu Leu Pro Gly Tyr Gln Val Pro Gly Ser Asp Leu Asn				
	340	345		350
Ser Cys Gln Leu Leu Tyr Pro Tyr Trp Ala Cys Trp Gly Tyr Trp His				
	355	360		365
Lys Tyr Gln Pro Leu Asp Gln Pro Leu Asp Lys Leu Ser Cys Leu Phe				
	370	375		380
Asp His Pro Gly Thr Val Phe Phe Ser Ile Phe Met Ser Phe Trp Gly				

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385		390		395		400
His Gly Leu Pro Gly Ala Leu Glu Ala Gly Ser Ala Thr Leu Ala His						
	405		410		415	
His Trp Asp Cys Ser Asp Phe Gln Asp Gln Glu Ala Met Pro Ser Ser						
	420		425		430	
Ala Pro His His Trp Asp Cys Ser Asp Phe Gln Asp Gln Glu Val Met						
	435		440		445	
Pro Ser Ser Ala Leu His His Trp Asp Cys Ser Asp Phe Gln Asp Gln						
	450		455		460	
Glu Glu Cys Pro His Leu Gln Phe Ala Ala Leu Ala Leu Gln Met Thr						
	465		470		475	480
Gln Asn Pro Val Thr Gly Leu Lys Glu Pro Tyr Phe Gln Pro His Ser						
	485		490		495	
Cys Leu Ser His Leu Leu Thr Ser Ser Ala Ala Ile Leu Thr Val Leu						
	500		505		510	
Cys Val Val Met Ile Phe Leu Val Ser Val Ile Ile Tyr His Gly Ile						
	515		520		525	
Ile Ser Ile Ala Met Phe His Thr Gly Asn Ser Val Leu Met Thr Gln						
	530		535		540	
Ala Asn Val Leu Trp Gly Asn Gly Gly Pro Lys Ala Leu Ser Lys Val						
	545		550		555	560
Leu Cys Val Cys Gln Gln Gln Cys Gly Pro Gly Gly Cys His Ile Gln						
	565		570		575	
Val Thr Gln Gln Leu Ile Ile Ile Met Val Gly Lys Gln Leu Leu Asn						
	580		585		590	
His Met Glu Glu Phe Val Gly Leu Gly Gly Gly Pro Gly Pro Asp Thr						
	595		600		605	
Pro Cys Leu Pro Glu Leu Gln Phe Gly Phe Ile Thr Ile Phe Val Gly						
	610		615		620	
Ala Phe Leu Leu Ala Pro Leu Phe Thr Leu Leu Asn Asn Arg Val Glu						
	625		630		635	640
Ile Gly Leu Asp Ala His Lys Phe Leu Cys Lys Tyr Gln Arg Pro Met						

645	650	655
Ala Gly Arg Gly Trp Thr Ser Gly Ser Asp Cys Ser Cys Trp Arg Pro		
660	665	670
Cys Glu Leu Ile Leu Pro Arg Thr Asn Ala Arg Ser Arg Leu Gly Tyr		
675	680	685
Trp Leu Asn Gly Gln Gly Gln Ile Leu Gly Arg Arg Arg Gly Gly Asn		
690	695	700
Ala Gly Phe Gly Val Glu Ile Arg Glu Pro Leu Gln Thr Pro Gln Pro		
705	710	715
Arg Tyr Lys Ala Ser Arg Asp Val Gly Val Asn Leu Ala Leu Phe Tyr		
725	730	735
Trp Lys Leu Leu Ala Val His Val His Leu Gly Phe Ile Ile Ala Phe		
740	745	750
Glu Gly Leu Met Asn Gln Thr Leu Cys Leu Gly Gly Ile Ser Pro Ser		
755	760	765
Gln Leu Gly Arg Glu Arg Ala Ser Pro Ala Gly Thr Ala Lys Gln His		
770	775	780
Gln Gln Arg Ala Trp Ala Gln Arg Gly Pro Gly Gly Trp Gln Ser Lys		
785	790	795
Arg Gly Met Asp Cys Gly Pro Pro Ala Thr Leu Gln Pro His Leu Thr		
805	810	815
Gly Pro Pro Gly Thr Ala His His Pro Val Ala Val Cys Gln Gln Glu		
820	825	830
Ser Leu Ser Phe Ala Glu Leu Pro Ala Leu Lys Pro Pro Ser Pro Val		
835	840	845
Cys Leu Asp Leu Phe Pro Val Ala Pro Glu Glu Leu Arg Ala Pro Gly		
850	855	860
Ser Arg Trp Ser Leu Gly Thr Pro Ala Pro Leu Gln Gly Leu Leu Trp		
865	870	875
Pro Leu Ser Pro Gly Gly Ser Asp Thr Glu Ile Thr Ser Gly Gly Met		
885	890	895
Arg Pro Ser Arg Ala Gly Ser Trp Pro His Cys Pro Gly Ala Gln Pro		

900	905	910
Pro Ala Leu Glu Gly Pro Trp Ser Pro Arg His Thr Gln Pro Gln Arg		
915	920	925
Arg Ala Ser His Gly Ser Glu Lys Lys Ser Ala Trp Arg Lys Met Arg		
930	935	940
Val Tyr Gln Arg Glu Glu Val Pro Gly Cys Pro Glu Ala His Ala Val		
945	950	955
Phe Leu Glu Pro Gly Gln Val Val Gln Glu Gln Ala Leu Ser Thr Glu		
965	970	975
Glu Pro Arg Val Glu Leu Ser Gly Ser Thr Arg Val Ser Leu Glu Gly		
980	985	990
Pro Glu Arg Arg Arg Phe Ser Ala Ser Glu Leu Met Thr Arg Leu His		
995	1000	1005
Ser Ser Leu Arg Leu Gly Arg Asn Ser Ala Ala Arg Ala Leu Ile Ser		
1010	1015	1020
Gly Ser Gly Thr Gly Ala Ala Arg Glu Gly Lys Ala Ser Gly Met Glu		
1025	1030	1035
Ala Arg Ser Val Glu Met Ser Gly Asp Arg Val Ser Arg Pro Ala Pro		
1045	1050	1055
Gly Asp Ser Arg Glu Gly Asp Trp Ser Glu Pro Arg Leu Asp Thr Gln		
1060	1065	1070
Glu Glu Pro Pro Leu Gly Ser Arg Ser Thr Asn Glu Arg Arg Gln Ser		
1075	1080	1085
Arg Phe Leu Leu Asn Ser Val Leu Tyr Gln Glu Tyr Ser Asp Val Ala		
1090	1095	1100
Ser Ala Arg Glu Leu Arg Arg Gln Gln Arg Glu Glu Glu Gly Pro Gly		
1105	1110	1115
Asp Glu Ala Glu Gly Ala Glu Glu Gly Pro Gly Pro Pro Arg Ala Asn		
1125	1130	1135
Leu Ser Pro Ser Ser Ser Phe Arg Ala Gln Arg Ser Ala Arg Gly Ser		
1140	1145	1150
Thr Phe Ser Leu Trp Gln Asp Ile Pro Asp Val Arg Gly Ser Gly Val		

1155	1160	1165
Leu Ala Thr Leu Ser Leu Arg Asp Cys Lys Leu Gln Glu Ala Lys Phe		
1170	1175	1180
Glu Leu Ile Thr Ser Glu Ala Ser Tyr Ile His Ser Leu Ser Val Ala		
1185	1190	1195 1200
Val Gly His Phe Leu Gly Ser Ala Glu Leu Ser Glu Cys Leu Gly Ala		
1205	1210	1215
Gln Asp Lys Gln Trp Leu Phe Ser Lys Leu Pro Glu Val Lys Ser Thr		
1220	1225	1230
Ser Glu Arg Phe Leu Gln Asp Leu Glu Gln Arg Leu Glu Ala Asp Val		
1235	1240	1245
Leu Arg Phe Ser Val Cys Asp Val Val Leu Asp His Cys Pro Ala Phe		
1250	1255	1260
Arg Arg Val Tyr Leu Pro Tyr Val Thr Asn Gln Ala Tyr Gln Glu Arg		
1265	1270	1275 1280
Thr Tyr Gln Arg Leu Leu Glu Asn Pro Arg Phe Pro Gly Ile Leu		
1285	1290	1295
Ala Arg Leu Glu Glu Ser Pro Val Cys Gln Arg Leu Pro Leu Thr Ser		
1300	1305	1310
Phe Leu Ile Leu Pro Phe Gln Arg Ile Thr Arg Leu Lys Met Leu Val		
1315	1320	1325
Glu Asn Ile Leu Lys Arg Thr Ala Gln Gly Ser Glu Asp Glu Asp Met		
1330	1335	1340
Ala Thr Lys Ala Phe Asn Ala Leu Lys Glu Leu Val Gln Glu Cys Asn		
1345	1350	1355 1360
Ala Ser Val Gln Ser Met Lys Arg Thr Glu Glu Leu Ile His Leu Ser		
1365	1370	1375
Lys Lys Ile His Phe Glu Gly Lys Ile Phe Pro Leu Ile Ser Gln Ala		
1380	1385	1390
Arg Trp Leu Val Arg His Gly Glu Leu Val Glu Leu Ala Pro Leu Pro		
1395	1400	1405
Ala Ala Pro Pro Ala Lys Leu Lys Leu Ser Ser Lys Ala Val Tyr Leu		

1410	1415	1420
His Leu Phe Asn Asp Cys Leu Leu Leu Ser Arg Arg Lys Glu Leu Gly		
1425	1430	1435 1440
Lys Phe Ala Val Phe Val His Ala Lys Met Ala Glu Leu Gln Val Arg		
1445	1450	1455
Asp Leu Ser Leu Lys Leu Gln Gly Ile Pro Gly His Val Phe Leu Leu		
1460	1465	1470
Gln Leu Leu His Gly Gln His Met Lys His Gln Phe Leu Leu Arg Ala		
1475	1480	1485
Arg Thr Glu Ser Glu Lys Gln Arg Trp Ile Ser Ala Leu Cys Pro Ser		
1490	1495	1500
Ser Pro Gln Glu Asp Lys Glu Val Ile Ser Glu Gly Glu Asp Cys Pro		
1505	1510	1515 1520
Gln Val Gln Cys Val Arg Thr Tyr Lys Ala Leu His Pro Asp Glu Leu		
1525	1530	1535
Thr Leu Glu Lys Thr Asp Ile Leu Ser Val Arg Thr Trp Thr Ser Asp		
1540	1545	1550
Gly Trp Leu Glu Gly Val Arg Leu Ala Asp Gly Glu Lys Gly Trp Val		
1555	1560	1565
Pro Gln Ala Tyr Val Glu Glu Ile Ser Ser Leu Ser Ala Arg Leu Arg		
1570	1575	1580
Asn Leu Arg Glu Asn Lys Arg Val Thr Ser Ala Thr Ser Lys Leu Gly		
1585	1590	1595 1600
Glu Ala Pro Val		

<210> 9
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(399)

<220>
 <221> misc_feature
 <222> (1)
 <223> wherein n may be a or t or g or c

<400> 9
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 Xaa Asp Asp Glu Gln Asn Met Ile Ser Ile Leu Ser Leu Val Ser Val
 1 5 10 15
 acc att gct gtg ttc atc cca gtt gcc tgt gac agt cat gat caa caa 96
 Thr Ile Ala Val Phe Ile Pro Val Ala Cys Asp Ser His Asp Gln Gln
 20 25 30
 gtc tgc acc atg acc ttc tca tct cca tat cca gtg ccc aag tta ttc 144
 Val Cys Thr Met Thr Phe Ser Ser Pro Tyr Pro Val Pro Lys Leu Phe
 35 40 45
 ctt tcc cca act gca ggc ccc cca aca gga tgt ggg cag cct gca tct 192
 Leu Ser Pro Thr Ala Gly Pro Pro Thr Gly Cys Gly Gln Pro Ala Ser
 50 55 60
 ccg ctg gac tgg agc caa aat gcc aaa gca cag cac ctt cga gtt cca 240
 Pro Leu Asp Trp Ser Gln Asn Ala Lys Ala Gln His Leu Arg Val Pro
 65 70 75 80
 tgc ctc cag aag ggc ttg tcc ctg cgc act ggg atg gtg ctt gtt tgc 288
 Cys Leu Gln Lys Gly Leu Ser Leu Arg Thr Gly Met Val Leu Val Cys
 85 90 95
 aag gtt ata gat gag aaa act gct gcc ttg tcg gaa gga aag gtg ctg 336
 Lys Val Ile Asp Glu Lys Thr Ala Ala Leu Ser Glu Gly Lys Val Leu
 100 105 110
 ttt ggt ctc ttc gct ggc atc ccc atc ttt agg aat tcc agc cca aac 384
 Phe Gly Leu Phe Ala Gly Ile Pro Ile Phe Arg Asn Ser Ser Pro Asn
 115 120 125
 aag ccg cct tcc aat tag 402
 Lys Pro Pro Ser Asn
 130

<210> 10
 <211> 133
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)..(133)
 <223> Wherein Xaa is any amino acid.

<400> 10

Xaa Asp Asp Glu Gln Asn Met Ile Ser Ile Leu Ser Leu Val Ser Val
 1 5 10 15

Thr Ile Ala Val Phe Ile Pro Val Ala Cys Asp Ser His Asp Gln Gln
 20 25 30

Val Cys Thr Met Thr Phe Ser Ser Pro Tyr Pro Val Pro Lys Leu Phe
 35 40 45

Leu Ser Pro Thr Ala Gly Pro Pro Thr Gly Cys Gly Gln Pro Ala Ser
 50 55 60

Pro Leu Asp Trp Ser Gln Asn Ala Lys Ala Gln His Leu Arg Val Pro
 65 70 75 80

Cys Leu Gln Lys Gly Leu Ser Leu Arg Thr Gly Met Val Leu Val Cys
 85 90 95

Lys Val Ile Asp Glu Lys Thr Ala Ala Leu Ser Glu Gly Lys Val Leu
 100 105 110

Phe Gly Leu Phe Ala Gly Ile Pro Ile Phe Arg Asn Ser Ser Pro Asn
 115 120 125

Lys Pro Pro Ser Asn
 130

<210> 11
 <211> 3825
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(3822)

<400> 11

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 Met Arg Ser Gly Arg His Pro Ser Leu Leu Leu Leu Val Leu Leu
 1 5 10 15

ctg tgg ctg ctg cag gtc agt atc att gac agt gtt caa cag gaa aca	96
Leu Trp Leu Leu Gln Val Ser Ile Ile Asp Ser Val Gln Gln Glu Thr	
20 25 30	
gat gat ctt act aag caa aca aag tgt cac tat aag ttc cag gaa aag	144
Asp Asp Leu Thr Lys Gln Thr Lys Cys His Tyr Lys Phe Gln Glu Lys	
35 40 45	
atc tac cag cct cta cgg cga tcc aag aga aga tgg gtt atc acc acc	192
Ile Tyr Gln Pro Leu Arg Arg Ser Lys Arg Arg Trp Val Ile Thr Thr	
50 55 60	
ttg gag ctg gag gag gaa gac ccg gga ccc ttt ccc aaa ctc att ggt	240
Leu Glu Leu Glu Glu Glu Asp Pro Gly Pro Phe Pro Lys Leu Ile Gly	
65 70 75 80	
gag ctg ttc aat aat atg tct tat aac atg tca cta atg tat cta atc	288
Glu Leu Phe Asn Asn Met Ser Tyr Asn Met Ser Leu Met Tyr Leu Ile	
85 90 95	
agt gga cct ggt gtg gat gaa tat cca gag att ggt ttg ttt tct cta	336
Ser Gly Pro Gly Val Asp Glu Tyr Pro Glu Ile Gly Leu Phe Ser Leu	
100 105 110	
gaa gat cat gag aac gga agg ata tat gtt cac cgc cct gtc gat cga	384
Glu Asp His Glu Asn Gly Arg Ile Tyr Val His Arg Pro Val Asp Arg	
115 120 125	
gaa atg aca cca tct ttc acg agc tgg aca gca agg gtg cct tcc tcc	432
Glu Met Thr Pro Ser Phe Thr Ser Trp Thr Ala Arg Val Pro Ser Ser	
130 135 140	
agg gct tcc gcg ggg atg agc aga ggc cat cta cgg gaa ggg ctg gtg	480
Arg Ala Ser Ala Gly Met Ser Arg Gly His Leu Arg Glu Gly Leu Val	
145 150 155 160	
ctg gtt tat ttt gat gtt gtg gag cgc tca aca gga aaa att gtg gat	528
Leu Val Tyr Phe Asp Val Val Glu Arg Ser Thr Gly Lys Ile Val Asp	
165 170 175	
aca tcc ttg att ttc aac att agg atc agt gat gtg aat gat cat gca	576
Thr Ser Leu Ile Phe Asn Ile Arg Ile Ser Asp Val Asn Asp His Ala	
180 185 190	
ccc cag ttt cca gag aag gaa ttt aac atc act gtg caa gaa aac caa	624
Pro Gln Phe Pro Glu Lys Glu Phe Asn Ile Thr Val Gln Glu Asn Gln	
195 200 205	

tct gca ggg caa cct att ttt cag atg tta gca gtc gat ttg gat gaa	672
Ser Ala Gly Gln Pro Ile Phe Gln Met Leu Ala Val Asp Leu Asp Glu	
210 215 220	
gaa aac act cca aat tct caa gtc ctt tac ttc ctc att tct caa aca	720
Glu Asn Thr Pro Asn Ser Gln Val Leu Tyr Phe Leu Ile Ser Gln Thr	
225 230 235 240	
cca tta ctg aaa gaa agt ggt ttc cgg gtt gat cgc ctt agt gga gaa	768
Pro Leu Leu Lys Glu Ser Gly Phe Arg Val Asp Arg Leu Ser Gly Glu	
245 250 255	
ata cga ctc tct ggc tgc tta gat tat gag acc gct cct cag ttt aca	816
Ile Arg Leu Ser Gly Cys Leu Asp Tyr Glu Thr Ala Pro Gln Phe Thr	
260 265 270	
ctg cta atc aga gcc agg gac tgt gga gaa ccg tca ctg tca tcc acg	864
Leu Leu Ile Arg Ala Arg Asp Cys Gly Glu Pro Ser Leu Ser Ser Thr	
275 280 285	
acc acc gtt cac gtg gat gtg caa gaa ggc aac aac cac agg cct gca	912
Thr Thr Val His Val Asp Val Gln Glu Gly Asn Asn His Arg Pro Ala	
290 295 300	
ttt acc cag gag aac tat aag gtt cag att cct gaa ggc cga gcc agc	960
Phe Thr Gln Glu Asn Tyr Lys Val Gln Ile Pro Glu Gly Arg Ala Ser	
305 310 315 320	
cag ggc gtg ttg cgt ctc ctg gtt caa gat cga gat tct cca ttt aca	1008
Gln Gly Val Leu Arg Leu Leu Val Gln Asp Arg Asp Ser Pro Phe Thr	
325 330 335	
tca gct tgg aga gca aaa ttc aac ata ttg cat ggc aat gaa gag ggg	1056
Ser Ala Trp Arg Ala Lys Phe Asn Ile Leu His Gly Asn Glu Glu Gly	
340 345 350	
cat ttt gac att tcg act gac cct gag acc aac gaa ggg ata tta aat	1104
His Phe Asp Ile Ser Thr Asp Pro Glu Thr Asn Glu Gly Ile Leu Asn	
355 360 365	
gtt atc aag cct ttg gat tat gag act cgc cca gcg caa agc ctc atc	1152
Val Ile Lys Pro Leu Asp Tyr Glu Thr Arg Pro Ala Gln Ser Leu Ile	
370 375 380	
att gtc gtg gag aat gag gag agg ctc gtc ttc tgt gag aga gga aag	1200
Ile Val Val Glu Asn Glu Glu Arg Leu Val Phe Cys Glu Arg Gly Lys	
385 390 395 400	

ctt cag ccg cca agg aag gca gca gcc agc gcc act gtg agt gtg cag	1248
Leu Gln Pro Pro Arg Lys Ala Ala Ala Ser Ala Thr Val Ser Val Gln	
405 410 415	
gtg aca gac gcc aac gac cca cca gcc ttt cac ccc cag agc ttc att	1296
Val Thr Asp Ala Asn Asp Pro Pro Ala Phe His Pro Gln Ser Phe Ile	
420 425 430	
gtc aat aaa gag gag ggc gcc agg cct ggg acc ctg ttg gga act ttt	1344
Val Asn Lys Glu Glu Gly Ala Arg Pro Gly Thr Leu Leu Gly Thr Phe	
435 440 445	
aat gcc atg gat cca gac agc cag ata aga tat gaa ctg gtt cat gac	1392
Asn Ala Met Asp Pro Asp Ser Gln Ile Arg Tyr Glu Leu Val His Asp	
450 455 460	
cca gca aat tgg gtc agc gtc gac aaa aac tcc gga gtg gtc atc acc	1440
Pro Ala Asn Trp Val Ser Val Asp Lys Asn Ser Gly Val Val Ile Thr	
465 470 475 480	
gtg gag cca att gac cga gaa tcc cct cat gta aat aac agt ttt tat	1488
Val Glu Pro Ile Asp Arg Glu Ser Pro His Val Asn Asn Ser Phe Tyr	
485 490 495	
gta atc atc att cac gct gtt gat gat ggc ttc cca ccg cag act gct	1536
Val Ile Ile Ile His Ala Val Asp Asp Gly Phe Pro Pro Gln Thr Ala	
500 505 510	
aca ggg acc cta atg ctc ttc ctg tct gac atc aat gac aac gtc ccg	1584
Thr Gly Thr Leu Met Leu Phe Leu Ser Asp Ile Asn Asp Asn Val Pro	
515 520 525	
act ctc cgg cca cgt tcc cgc tac atg gag gtc tgt gag tct gct gtg	1632
Thr Leu Arg Pro Arg Ser Arg Tyr Met Glu Val Cys Glu Ser Ala Val	
530 535 540	
cat gag ccc ctc cac atc gag gca gag gat ccg gac ctg gag ccg ttc	1680
His Glu Pro Leu His Ile Glu Ala Glu Asp Pro Asp Leu Glu Pro Phe	
545 550 555 560	
tct gac cca ttt aca ttt gaa ttg gac aat acc tgg gga aat gcg gag	1728
Ser Asp Pro Phe Thr Phe Glu Leu Asp Asn Thr Trp Gly Asn Ala Glu	
565 570 575	
gac aca tgg aag ttg ggg aga aat tgg gga aac tct cct cat cag ggg	1776
Asp Thr Trp Lys Leu Gly Arg Asn Trp Gly Asn Ser Pro His Gln Gly	
580 585 590	

gta gga ggc tgc tgg gag tcc ctg aga cat att ctt gca tct ggc aag	1824
Val Gly Gly Cys Trp Glu Ser Leu Arg His Ile Leu Ala Ser Gly Lys	
595 600 605	
aag ggt gtt tcc agg gaa gct cca gga ttg acg tca ctg ttt ggc ctg	1872
Lys Gly Val Ser Arg Glu Ala Pro Gly Leu Thr Ser Leu Phe Gly Leu	
610 615 620	
ggt caa tca gtt gaa ctt tta acc ttg aga agc ctg cca cgt ggt aat	1920
Gly Gln Ser Val Glu Leu Leu Thr Leu Arg Ser Leu Pro Arg Gly Asn	
625 630 635 640	
tac ttg gtg cca ctc ttc att gga gac aaa cag gga ctt tcc cag aag	1968
Tyr Leu Val Pro Leu Phe Ile Gly Asp Lys Gln Gly Leu Ser Gln Lys	
645 650 655	
caa act gtc cat gta agg atc tgc ccc tgt gcc agt ggg ctc aca tgt	2016
Gln Thr Val His Val Arg Ile Cys Pro Cys Ala Ser Gly Leu Thr Cys	
660 665 670	
gtg gag ctt gca gat gca gaa gtg ggg ctt cat gtg ggg gcc ctg ttc	2064
Val Glu Leu Ala Asp Ala Glu Val Gly Leu His Val Gly Ala Leu Phe	
675 680 685	
cct gtc tgt gca gca ttt gtg gct ctg gca gtg gct ctg ctt ttt ctg	2112
Pro Val Cys Ala Ala Phe Val Ala Leu Ala Val Ala Leu Leu Phe Leu	
690 695 700	
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Leu Arg Cys Tyr Phe Val Leu Glu Pro Lys Arg His Gly Cys Ser Val	
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Ser Asn Asp Glu Gly His Gln Thr Leu Val Met Tyr Asn Ala Glu Ser	
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Lys Gly Thr Ser Ala Gln Thr Trp Ser Asp Val Glu Gly Gln Arg Pro	
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Gly Arg Glu Pro Lys Pro Pro Pro Ser Arg Phe Trp Cys Ile Ser Gly	
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Phe Pro Ser Val Ser Cys Lys Tyr Cys Arg Ser Arg Gly Ser Ala Ser	
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Asp Ser Thr Glu Thr Gln Ile His Arg His Gly Pro Asp Glu Gln Glu	
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Thr Ala Ser Ser Pro Ser Trp Glu Thr Met Gly Ser Pro Ala Glu Trp	
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Ala Val Tyr Pro Gln Thr Gln Gly Cys Arg Ala Leu Pro Gln Val Leu	
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Thr Ala Glu Leu Glu Met Gly Leu Glu Asp Arg Glu Arg Thr Glu Ala	
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Leu Gly Glu Ala Phe Met Ala Arg Leu Ala Ala Asp Leu Lys Gly Asp	
915 920 925	
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Tyr Leu Gln Ser Leu Gly Arg Glu Ala Ser Thr Val Glu Ser Cys Val	
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Gly Arg Ser Gln Ser Pro Ser His Trp Gln Ala Lys Lys Ala Trp Ile	
945 950 955 960	
ccc aaa ctt tta caa aag aga aat aaa ttc aac aac gta gca cct ata	2928
Pro Lys Leu Leu Gln Lys Arg Asn Lys Phe Asn Asn Val Ala Pro Ile	
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Val Asn Asn Val Ala Ser Ile Val Asn Asn Ile Ala Pro Ile Val Asn	
980 985 990	
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Asn Val Ala Pro Ile Val Asn Asn Val Ala Ser Ile Val Asn Asn Val	
995 1000 1005	
gca cct ata gtc aac aac gta gca cct ata gtc aac aac ata gca cct	3072
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Thr Leu Ser Ala Arg Ile His Val Gln Lys Val Gln Ser Lys Glu Arg	
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1075 1080 1085	
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Arg Arg Leu Thr Gln Thr Gly Lys Arg Lys His Gly Ala Leu Ala Arg	
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Thr Pro Ser Phe Lys Lys Val Val Tyr Asp His Lys Glu Val Ser Leu	
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Trp Ile Arg Thr His Gln Trp Phe Pro Ser Ala Trp Glu Phe Pro Phe	
1140 1145 1150	
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Asn Gly Leu Arg Thr Met Ser Leu Pro Phe Leu Pro Glu Ala Gln Asn	
1155 1160 1165	

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Ala Phe Ala Tyr Ser Val Pro Ser Ser Trp Ser Pro Val Pro Thr Pro
1185 1190 1195 1200

atc tac aga aac tcc acc agc cct cct ggc tgc ccc gat ggt cct cgc 3648
Ile Tyr Arg Asn Ser Thr Ser Pro Pro Gly Cys Pro Asp Gly Pro Arg
1205 1210 1215

aca ggg aga ctt gtc tac ctc ccg agg tca cgt gtg ggc tct ggt cct 3696
Thr Gly Arg Leu Val Tyr Leu Pro Arg Ser Arg Val Gly Ser Gly Pro
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ctt gcc atc atg gca gag att ttg ctg tat ctc ccc ctg gct gct ggt 3744
Leu Ala Ile Met Ala Glu Ile Leu Leu Tyr Leu Pro Leu Ala Ala Gly
1235 1240 1245

gct ctg ctt acc tcc tcc aga gtt gtt aac aaa gag ctg agg atg ctg 3792
Ala Leu Leu Thr Ser Ser Arg Val Val Asn Lys Glu Leu Arg Met Leu
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agc tgc cca ggg act tgg ctg cag gtg gca tag 3825
Ser Cys Pro Gly Thr Trp Leu Gln Val Ala
1265 1270

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Leu Trp Leu Leu Gln Val Ser Ile Ile Asp Ser Val Gln Gln Glu Thr
20 25 30

Asp Asp Leu Thr Lys Gln Thr Lys Cys His Tyr Lys Phe Gln Glu Lys
35 40 45

Ile Tyr Gln Pro Leu Arg Arg Ser Lys Arg Arg Trp Val Ile Thr Thr
50 55 60

Leu Glu Leu Glu Glu Glu Asp Pro Gly Pro Phe Pro Lys Leu Ile Gly

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65		70		75		80									
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Ser	Gly	Pro	Gly	Val	Asp	Glu	Tyr	Pro	Glu	Ile	Gly	Leu	Phe	Ser	Leu
		100						105				110			
Glu	Asp	His	Glu	Asn	Gly	Arg	Ile	Tyr	Val	His	Arg	Pro	Val	Asp	Arg
		115					120					125			
Glu	Met	Thr	Pro	Ser	Phe	Thr	Ser	Trp	Thr	Ala	Arg	Val	Pro	Ser	Ser
	130					135					140				
Arg	Ala	Ser	Ala	Gly	Met	Ser	Arg	Gly	His	Leu	Arg	Glu	Gly	Leu	Val
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Leu	Val	Tyr	Phe	Asp	Val	Val	Glu	Arg	Ser	Thr	Gly	Lys	Ile	Val	Asp
			165					170					175		
Thr	Ser	Leu	Ile	Phe	Asn	Ile	Arg	Ile	Ser	Asp	Val	Asn	Asp	His	Ala
		180						185					190		
Pro	Gln	Phe	Pro	Glu	Lys	Glu	Phe	Asn	Ile	Thr	Val	Gln	Glu	Asn	Gln
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Ser	Ala	Gly	Gln	Pro	Ile	Phe	Gln	Met	Leu	Ala	Val	Asp	Leu	Asp	Glu
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Pro	Leu	Leu	Lys	Glu	Ser	Gly	Phe	Arg	Val	Asp	Arg	Leu	Ser	Gly	Glu
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Ile	Arg	Leu	Ser	Gly	Cys	Leu	Asp	Tyr	Glu	Thr	Ala	Pro	Gln	Phe	Thr
		260					265						270		
Leu	Leu	Ile	Arg	Ala	Arg	Asp	Cys	Gly	Glu	Pro	Ser	Leu	Ser	Ser	Thr
		275				280						285			
Thr	Thr	Val	His	Val	Asp	Val	Gln	Glu	Gly	Asn	Asn	His	Arg	Pro	Ala
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Phe	Thr	Gln	Glu	Asn	Tyr	Lys	Val	Gln	Ile	Pro	Glu	Gly	Arg	Ala	Ser
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Gln	Gly	Val	Leu	Arg	Leu	Leu	Val	Gln	Asp	Arg	Asp	Ser	Pro	Phe	Thr

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Ser Ala Trp Arg Ala Lys Phe Asn Ile Leu His Gly Asn Glu Glu Gly		
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His Phe Asp Ile Ser Thr Asp Pro Glu Thr Asn Glu Gly Ile Leu Asn		
355	360	365
Val Ile Lys Pro Leu Asp Tyr Glu Thr Arg Pro Ala Gln Ser Leu Ile		
370	375	380
Ile Val Val Glu Asn Glu Glu Arg Leu Val Phe Cys Glu Arg Gly Lys		
385	390	395
Leu Gln Pro Pro Arg Lys Ala Ala Ala Ser Ala Thr Val Ser Val Gln		
405	410	415
Val Thr Asp Ala Asn Asp Pro Pro Ala Phe His Pro Gln Ser Phe Ile		
420	425	430
Val Asn Lys Glu Glu Gly Ala Arg Pro Gly Thr Leu Leu Gly Thr Phe		
435	440	445
Asn Ala Met Asp Pro Asp Ser Gln Ile Arg Tyr Glu Leu Val His Asp		
450	455	460
Pro Ala Asn Trp Val Ser Val Asp Lys Asn Ser Gly Val Val Ile Thr		
465	470	475
Val Glu Pro Ile Asp Arg Glu Ser Pro His Val Asn Asn Ser Phe Tyr		
485	490	495
Val Ile Ile Ile His Ala Val Asp Asp Gly Phe Pro Pro Gln Thr Ala		
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Thr Gly Thr Leu Met Leu Phe Leu Ser Asp Ile Asn Asp Asn Val Pro		
515	520	525
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530	535	540
His Glu Pro Leu His Ile Glu Ala Glu Asp Pro Asp Leu Glu Pro Phe		
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Ser Asp Pro Phe Thr Phe Glu Leu Asp Asn Thr Trp Gly Asn Ala Glu		
565	570	575
Asp Thr Trp Lys Leu Gly Arg Asn Trp Gly Asn Ser Pro His Gln Gly		

580	585	590
Val Gly Gly Cys Trp Glu Ser Leu Arg His Ile Leu Ala Ser Gly Lys		
595	600	605
Lys Gly Val Ser Arg Glu Ala Pro Gly Leu Thr Ser Leu Phe Gly Leu		
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Gly Gln Ser Val Glu Leu Leu Thr Leu Arg Ser Leu Pro Arg Gly Asn		
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Tyr Leu Val Pro Leu Phe Ile Gly Asp Lys Gln Gly Leu Ser Gln Lys		
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Gln Thr Val His Val Arg Ile Cys Pro Cys Ala Ser Gly Leu Thr Cys		
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Val Glu Leu Ala Asp Ala Glu Val Gly Leu His Val Gly Ala Leu Phe		
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Leu Arg Cys Tyr Phe Val Leu Glu Pro Lys Arg His Gly Cys Ser Val		
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Ser Asn Asp Glu Gly His Gln Thr Leu Val Met Tyr Asn Ala Glu Ser		
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Lys Gly Thr Ser Ala Gln Thr Trp Ser Asp Val Glu Gly Gln Arg Pro		
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Ala Leu Leu Ile Cys Thr Ala Ala Ala Gly Pro Thr Gln Gly Val Lys		
755	760	765
Gly Arg Glu Pro Lys Pro Pro Pro Ser Arg Phe Trp Cys Ile Ser Gly		
770	775	780
Phe Pro Ser Val Ser Cys Lys Tyr Cys Arg Ser Arg Gly Ser Ala Ser		
785	790	795
Ile Cys Ser Glu Ser Val Ser Pro Ser Thr Leu Cys Ser Gly Glu Leu		
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Asp Ser Thr Glu Thr Gln Ile His Arg His Gly Pro Asp Glu Gln Glu		
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Thr Ala Ser Ser Pro Ser Trp Glu Thr Met Gly Ser Pro Ala Glu Trp		

835	840	845
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Leu Gly Glu Ala Phe Met Ala Arg Leu Ala Ala Asp Leu Lys Gly Asp		
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Tyr Leu Gln Ser Leu Gly Arg Glu Ala Ser Thr Val Glu Ser Cys Val		
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Gly Arg Ser Gln Ser Pro Ser His Trp Gln Ala Lys Lys Ala Trp Ile		
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Pro Lys Leu Leu Gln Lys Arg Asn Lys Phe Asn Asn Val Ala Pro Ile		
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Ala Pro Ile Val Asn Asn Val Ala Pro Ile Val Asn Asn Ile Ala Pro		
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Ile Val Asn Asn Val Ala Ser Ile Val Asn Asn Ala Leu Gln His Phe		
1025	1030	1035 1040
Thr Leu Ser Ala Arg Ile His Val Gln Lys Val Gln Ser Lys Glu Arg		
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Asn Arg Phe Ser Leu Ser Arg Gly Cys Ile Ile Pro Gln Gly Arg Ala		
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Thr Ala Gly Arg Gly Leu Pro Gln Asp Ile Tyr Lys Glu Met Met Pro		
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Thr Pro Ser Phe Lys Lys Val Val Tyr Asp His Lys Glu Val Ser Leu		
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Ile Cys Trp Val Gln Thr Ser Pro Glu Asp Pro Pro Pro His Ile Pro		
	1125	1130 1135
Trp Ile Arg Thr His Gln Trp Phe Pro Ser Ala Trp Glu Phe Pro Phe		
	1140	1145 1150
Asn Gly Leu Arg Thr Met Ser Leu Pro Phe Leu Pro Glu Ala Gln Asn		
	1155	1160 1165
Pro Ser Tyr Arg Ser Leu Pro Gln Arg Pro Ser Trp Ala Ser Leu Gln		
	1170	1175 1180
Ala Phe Ala Tyr Ser Val Pro Ser Ser Trp Ser Pro Val Pro Thr Pro		
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aga gcc cct gtg cct ctc cct gca gct ggc tgg gag ttc cag ggc att	144			
Arg Ala Pro Val Pro Leu Pro Ala Ala Gly Trp Glu Phe Gln Gly Ile				
35	40	45		
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Asn Thr Asp Ser Leu Cys Pro Ser Ala Ser Asp Cys Met Glu Leu Gly				
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tgt gaa tac aca gct cct gca tcc ctc cga ggc atc tcc aca ccg tct	240			
Cys Glu Tyr Thr Ala Pro Ala Ser Leu Arg Gly Ile Ser Thr Pro Ser				
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ccc aga gaa tgt ctc gta aaa gct gct cct ctt ggg gag gct ctg ggc	288			
Pro Arg Glu Cys Leu Val Lys Ala Ala Pro Leu Gly Glu Ala Leu Gly				
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Phe Gly Glu Ser Thr Trp Asn Ser Pro Leu Glu Lys Pro Lys Asn				
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<211> 111				
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Arg Ala Pro Val Pro Leu Pro Ala Ala Gly Trp Glu Phe Gln Gly Ile				
35	40	45		
Asn Thr Asp Ser Leu Cys Pro Ser Ala Ser Asp Cys Met Glu Leu Gly				
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Cys Glu Tyr Thr Ala Pro Ala Ser Leu Arg Gly Ile Ser Thr Pro Ser				
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Phe Gly Glu Ser Thr Trp Asn Ser Pro Leu Glu Lys Pro Lys Asn
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<212> DNA
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Val Thr Pro Gly Leu Pro Ala Met Lys Leu Leu Tyr Leu Phe Leu Ala
20 25 30
atc ctt ctg gcc ata gaa gaa cca gtg ata tca gta gag tgt tgg atg 144
Ile Leu Leu Ala Ile Glu Glu Pro Val Ile Ser Val Glu Cys Trp Met
35 40 45
gat gga cac tgc cgg ttg ttg tgc aaa gat ggt gaa gac agc atc ata 192
Asp Gly His Cys Arg Leu Leu Cys Lys Asp Gly Glu Asp Ser Ile Ile
50 55 60
cgc tgc cga aat cgt aaa cgg tgc tgt gtt cct agt cgt tat tta aca 240
Arg Cys Arg Asn Arg Lys Arg Cys Cys Val Pro Ser Arg Tyr Leu Thr
65 70 75 80
atc caa cca gta aca att cat gga atc ctt ggc tgg acc act cct cag 288
Ile Gln Pro Val Thr Ile His Gly Ile Leu Gly Trp Thr Thr Pro Gln
85 90 95
atg tcc aca aca gct cca aaa atg aag aca aat ata act aat aga tag 336
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100 105 110

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<211> 111

<212> PRT

<213> Homo sapiens

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Ile Leu Leu Ala Ile Glu Glu Pro Val Ile Ser Val Glu Cys Trp Met
35 40 45

Asp Gly His Cys Arg Leu Leu Cys Lys Asp Gly Glu Asp Ser Ile Ile
50 55 60

Arg Cys Arg Asn Arg Lys Arg Cys Cys Val Pro Ser Arg Tyr Leu Thr
65 70 75 80

Ile Gln Pro Val Thr Ile His Gly Ile Leu Gly Trp Thr Thr Pro Gln
85 90 95

Met Ser Thr Thr Ala Pro Lys Met Lys Thr Asn Ile Thr Asn Arg
100 105 110

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<212> DNA

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<222> (1)..(138)

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cct ccc cgc att ctg gcc cag tgc tgc ttg gtc act ctg gct gtg cct 96
Pro Pro Arg Ile Leu Ala Gln Cys Cys Leu Val Thr Leu Ala Val Pro
20 25 30

cca gca ggc cca gct ctc aac gct ggc tgc acg gtc aag acc tag 141
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 Pro Ala Gly Pro Ala Leu Asn Ala Gly Cys Thr Val Lys Thr
 35 40 45

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 tca ctg cta tcc ttc tct tcc cct aca gta ggg ttt ctg gac tgc ggc 96
 Ser Leu Leu Ser Phe Ser Ser Pro Thr Val Gly Phe Leu Asp Cys Gly
 20 25 30
 aca gtt gtc act tca gac cag gta agg gct cta tta att atg ttc tat 144
 Thr Val Val Thr Ser Asp Gln Val Arg Ala Leu Leu Ile Met Phe Tyr
 35 40 45
 gaa tca caa tca gat tta aaa aca aac aaa aat aaa aca aaa caa aaa 192
 Glu Ser Gln Ser Asp Leu Lys Thr Asn Lys Asn Lys Thr Lys Gln Lys
 50 55 60
 caa aaa aga gaa ggg aag gag cgg tct gtg aac gtt aac aaa tgg aaa 240
 Gln Lys Arg Glu Gly Lys Glu Arg Ser Val Asn Val Asn Lys Trp Lys
 65 70 75 80
 tcc act ggg gat cag cct ctg tca gaa cta agc tcc agg aag gag gag 288

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Val Gln Pro Val Glu Glu Pro Val Ser Leu Ser Glu Gly Asn Leu Gly
      100                      105                      110

aaa agc aag aag gtg atg aag aat gag agg gag gaa gaa aag aag gaa 384
Lys Ser Lys Lys Val Met Lys Asn Glu Arg Glu Glu Glu Lys Lys Glu
      115                      120                      125

aag gaa caa act tcc agc ttc tca caa ttc cct tct gaa aga cgt aca 432
Lys Glu Gln Thr Ser Ser Phe Ser Gln Phe Pro Ser Glu Arg Arg Thr
      130                      135                      140

ctg ccc atg gca agg cac gct gga tat ggg tta agt aac ccc aat ctg 480
Leu Pro Met Ala Arg His Ala Gly Tyr Gly Leu Ser Asn Pro Asn Leu
      145                      150                      155                      160

aaa atc caa aat cca aaa tgc tac aac atc cca aat gtt ttg agt gcc 528
Lys Ile Gln Asn Pro Lys Cys Tyr Asn Ile Pro Asn Val Leu Ser Ala
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aat gtg atg atc aat gga aat gtt cac tag 558
Asn Val Met Ile Asn Gly Asn Val His
      180                      185

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<213> Homo sapiens

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      20                      25                      30

Thr Val Val Thr Ser Asp Gln Val Arg Ala Leu Leu Ile Met Phe Tyr
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Glu Ser Gln Ser Asp Leu Lys Thr Asn Lys Asn Lys Thr Lys Gln Lys
      50                      55                      60

Gln Lys Arg Glu Gly Lys Glu Arg Ser Val Asn Val Asn Lys Trp Lys
      65                      70                      75                      80

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Ser Thr Gly Asp Gln Pro Leu Ser Glu Leu Ser Ser Arg Lys Glu Glu
85 90 95

Val Gln Pro Val Glu Glu Pro Val Ser Leu Ser Glu Gly Asn Leu Gly
100 105 110

Lys Ser Lys Lys Val Met Lys Asn Glu Arg Glu Glu Glu Lys Lys Glu
115 120 125

Lys Glu Gln Thr Ser Ser Phe Ser Gln Phe Pro Ser Glu Arg Arg Thr
130 135 140

Leu Pro Met Ala Arg His Ala Gly Tyr Gly Leu Ser Asn Pro Asn Leu
145 150 155 160

Lys Ile Gln Asn Pro Lys Cys Tyr Asn Ile Pro Asn Val Leu Ser Ala
165 170 175

Asn Val Met Ile Asn Gly Asn Val His
180 185

<210> 21
<211> 1216
<212> DNA
<213> Homo sapiens

<400> 21
atgcggaggc cgagcgtgcg cgcggccggg ctggtcctgt gcaccctgtg ttacctgctg 60
gtgggcgctg ctgtcttcga cgcgctcgag tccgagggcg aaagcggccg ccagcgactg 120
ctggtccaga agcggggcgc tctccggagg aagtccggct tctcggccga ggactaccgc 180
gagctggagc gcctggcgct ccaggctgag cccacccgcg ccggccgcca gtggaagtgc 240
cccggctcct tctacttcgc catcaccgtc atcactacca tcgagtacgg ccacgccgcg 300
ccgggtacgg actccggcaa ggtcttctgc atgttctacg cgctcctggg catcccgtg 360
acgctggtca ctttccagag cctgggcgaa cggtgaacg cgggtggtgcg ggcctcctg 420
ttggcggcca agtgetgect gggcctgcgg tggacgtgcg tgtccacgga gaacctggtg 480
gtggccgggc tgctggcgtg tgccgccacc ctggccctcg gggccgtcgc cttctcgcac 540
ttcgagggtt ggacattctt ccacgcctac tactactgct tcatcaccct caccaccatc 600

ggcttcggcg acttcgtggc actgcagagc ggcgaggcgc tgcagaggaa gctcccctac 660
 gtggccttca gcttcctcta catcctcctg ggggtcacgg tcattggcgc cttcctcaac 720
 ctggtggtcc tgcgcttcct cgttgccagc gccgactggc ccgagcgcgc tgcccgcacc 780
 cccagcccgc gccccccggg ggcgcccag agccgtggcc tctggctgcc ccgccgccc 840
 gcccgtccg tgggctccgc ctctgtcttc tgccacgtgc acaagctgga gaggtgcgcc 900
 cgcgacaacc tgggcttttc gccccctcg agcccggggg tcgtgcgtgg cgggcaggct 960
 cccaggcttg gggcccgggtg gaagtccatc tgacaacccc acccaggcca gggtcgaatc 1020
 tggaatggga gggctctggct tcagctatca gggcacccctc cccagggatt ggaaacggat 1080
 gacgggcctt taggcggttt ttgcccagc gcagtttttc attactgtct gtggctaagt 1140
 cccctccctc ctttccaaaa atatattaca gtcaccccat aagcccaaaa aaaaaaaaaa 1200
 aaaaaaaaaa aaaaaa 1216

<210> 22
 <211> 393
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (340)
 <223> Wherein Xaa is any amino acid as defined in the
 specification

<400> 22
 Met Arg Arg Pro Ser Val Arg Ala Ala Gly Leu Val Leu Cys Thr Leu
 1 5 10 15
 Cys Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu
 20 25 30
 Ala Glu Ser Gly Arg Gln Arg Leu Leu Val Gln Lys Arg Gly Ala Leu
 35 40 45
 Arg Arg Lys Phe Gly Phe Ser Ala Glu Asp Tyr Arg Glu Leu Glu Arg
 50 55 60

Leu	Ala	Leu	Gln	Ala	Glu	Pro	His	Arg	Ala	Gly	Arg	Gln	Trp	Lys	Phe	
65					70					75					80	
Pro	Gly	Ser	Phe	Tyr	Phe	Ala	Ile	Thr	Val	Ile	Thr	Thr	Ile	Glu	Tyr	
			85						90					95		
Gly	His	Ala	Ala	Pro	Gly	Thr	Asp	Ser	Gly	Lys	Val	Phe	Cys	Met	Phe	
		100						105					110			
Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Thr	Leu	Val	Thr	Phe	Gln	Ser	Leu	
	115						120					125				
Gly	Glu	Arg	Leu	Asn	Ala	Val	Val	Arg	Arg	Leu	Leu	Leu	Ala	Ala	Lys	
	130					135					140					
Cys	Cys	Leu	Gly	Leu	Arg	Trp	Thr	Cys	Val	Ser	Thr	Glu	Asn	Leu	Val	
145					150					155					160	
Val	Ala	Gly	Leu	Leu	Ala	Cys	Ala	Ala	Thr	Leu	Ala	Leu	Gly	Ala	Val	
			165						170					175		
Ala	Phe	Ser	His	Phe	Glu	Gly	Trp	Thr	Phe	Phe	His	Ala	Tyr	Tyr	Tyr	
		180						185					190			
Cys	Phe	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Phe	Val	Ala	Leu	
	195						200					205				
Gln	Ser	Gly	Glu	Ala	Leu	Gln	Arg	Lys	Leu	Pro	Tyr	Val	Ala	Phe	Ser	
	210					215					220					
Phe	Leu	Tyr	Ile	Leu	Leu	Gly	Leu	Thr	Val	Ile	Gly	Ala	Phe	Leu	Asn	
225				230					235						240	
Leu	Val	Val	Leu	Arg	Phe	Leu	Val	Ala	Ser	Ala	Asp	Trp	Pro	Glu	Arg	
			245					250						255		
Ala	Ala	Arg	Thr	Pro	Ser	Pro	Arg	Pro	Pro	Gly	Ala	Pro	Glu	Ser	Arg	
		260						265					270			
Gly	Leu	Trp	Leu	Pro	Arg	Arg	Pro	Ala	Arg	Ser	Val	Gly	Ser	Ala	Ser	
	275					280						285				
Val	Phe	Cys	His	Val	His	Lys	Leu	Glu	Arg	Cys	Ala	Arg	Asp	Asn	Leu	
	290					295					300					
Gly	Phe	Ser	Pro	Pro	Ser	Ser	Pro	Gly	Val	Val	Arg	Gly	Gly	Gln	Ala	
305					310					315					320	

Pro Arg Leu Gly Ala Arg Trp Lys Ser Ile Xaa Gln Pro His Pro Gly
 325 330 335

Gln Gly Arg Ile Trp Asn Gly Arg Val Trp Leu Gln Leu Ser Gly His
 340 345 350

Pro Pro Gln Gly Leu Glu Thr Asp Asp Gly Pro Leu Gly Gly Phe Leu
 355 360 365

Pro Arg Ala Val Phe His Tyr Cys Leu Trp Leu Ser Pro Leu Pro Pro
 370 375 380

Phe Gln Lys Tyr Ile Thr Val Thr Pro
 385 390

<210> 23
 <211> 759
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> (1)
 <223> Wherein n is any nucleic acid as defined in the
 specification

<400> 23
 natcagactc tattgaccgc cactctaacg ttgtcaggca ttgtggcaat tgtgtccttg 60
 tggctttggg catttaagct tcactacttg acctctatag ttttggcatc ttctcataca 120
 catgactatc agcaagctaa attatttact gactgtcctg ctccccgcac tccgcctttg 180
 aggcgcggaa cgaagtggca cgcccgatc ccagctgatc agcggctggg ctttggcggt 240
 ggctcccccg ggcgagacca ttgtgactcc tcgggagggg cgcacgccgg ggagggggcg 300
 gagcggccat tgtccggtca ggcagacctc cgggggaggg gacggtgtta cggagacagc 360
 agggccccgg gcttcagagc ggccgctgcg actccggagc cggcgggggg ctccggtcct 420
 tccctgcgcc accgcacagg acatctctct ggctggggag cggcgggtgag acccgccgag 480
 gggtctgtgt tccctcctcc cccgcgggtc tcgagcgggg cccggggcca gccgcgcga 540
 ccgctgccgc cgccgagctc cgccgccgcc gagcaccatg ggagacgctg ggagcgagcg 600

cagcaaagcg cccagcctgc cgctcgctg tccctgcggc ttctggggac taacggcagt 660
 tccttttagga ttgctgctct ttcgagtgac ttaggctgca ggacttgctg cccagcattg 720
 cccagtcagg acactaatca gtgtggctcg gttgaatag 759

<210> 24

<211> 252

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)

<223> Wherein Xaa is any amino acid as defined in the
 specification

<400> 24

Xaa Gln Thr Leu Leu Thr Ala Thr Leu Thr Leu Ser Gly Ile Val Ala
 1 5 10 15

Ile Val Ser Leu Trp Leu Trp Ala Phe Lys Leu His Tyr Leu Thr Ser
 20 25 30

Ile Val Leu Ala Ser Ser His Thr His Asp Tyr Gln Gln Ala Lys Leu
 35 40 45

Phe Thr Asp Cys Pro Ala Pro Arg Thr Pro Pro Leu Arg Arg Gly Thr
 50 55 60

Lys Trp His Ala Arg Ile Pro Ala Asp Gln Arg Leu Gly Phe Gly Val
 65 70 75 80

Gly Ser Pro Gly Arg Asp His Cys Asp Ser Ser Gly Gly Ala His Ala
 85 90 95

Gly Glu Gly Ala Glu Arg Pro Leu Ser Gly Gln Arg Ser Leu Arg Gly
 100 105 110

Arg Gly Arg Cys Tyr Gly Asp Ser Arg Ala Arg Gly Phe Arg Ala Ala
 115 120 125

Ala Ala Thr Pro Glu Pro Ala Gly Gly Ser Gly Pro Ser Leu Arg His
 130 135 140

Arg Thr Gly His Leu Ser Gly Trp Gly Ala Ala Val Arg Pro Ala Glu
 145 150 155 160

Gly Val Cys Val Pro Pro Pro Pro Arg Ser Ser Ser Gly Ala Arg Ala
165 170 175

Gln Pro Pro Pro Pro Leu Pro Pro Pro Ser Ser Ala Ala Ala Glu His
180 185 190

His Gly Arg Arg Trp Glu Arg Ala Gln Gln Ser Ala Gln Pro Ala Ala
195 200 205

Ser Leu Ser Leu Arg Leu Leu Gly Thr Asn Gly Ser Ser Phe Arg Ile
210 215 220

Ala Ala Leu Ser Ser Asp Leu Gly Cys Arg Thr Cys Cys Pro Ala Leu
225 230 235 240

Pro Ser Gln Asp Thr Asn Gln Cys Gly Ser Val Glu
245 250

<210> 25
<211> 939
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(936)

<400> 25
atg cgg cat ccg ctg gtc ctg ctg ctg ctc ctc tct gcc ctg gtg acc 48
Met Arg His Pro Leu Val Leu Leu Leu Leu Leu Ser Ala Leu Val Thr
1 5 10 15

tcc ttc act gca gcc tct atc cac gat gct cat gcc caa gag agc tcc 96
Ser Phe Thr Ala Ala Ser Ile His Asp Ala His Ala Gln Glu Ser Ser
20 25 30

ttg ggt ctt aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt 144
Leu Gly Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu
35 40 45

ttc ctg aaa gat gac ctg ctt cgg ggc ata gac agc ttc ttc tct gcc 192
Phe Leu Lys Asp Asp Leu Leu Arg Gly Ile Asp Ser Phe Phe Ser Ala
50 55 60

ccc atg gac ttc cgg ggc ctc cct agg aac tac caa caa gag gag aac 240
Pro Met Asp Phe Arg Gly Leu Pro Arg Asn Tyr Gln Gln Glu Glu Asn

65				70				75				80				
gag	gag	cac	cag	ctg	agg	aac	aac	acc	ctc	tcc	agc	cac	ctc	cat	att	288
Glu	Glu	His	Gln	Leu	Arg	Asn	Asn	Thr	Leu	Ser	Ser	His	Leu	His	Ile	
85				90				95								
gac	aag	gtg	acc	gac	aat	aag	aca	gga	gag	gtg	ctg	atc	tcc	gag	aag	336
Asp	Lys	Val	Thr	Asp	Asn	Lys	Thr	Gly	Glu	Val	Leu	Ile	Ser	Glu	Lys	
100				105				110								
gtg	gtg	gca	tcc	atc	cag	ccg	gcg	gag	ggg	agc	ttc	gag	ggg	aac	tgg	384
Val	Val	Ala	Ser	Ile	Gln	Pro	Ala	Glu	Gly	Ser	Phe	Glu	Gly	Asn	Trp	
115				120				125								
aag	gcg	gcg	gcc	ctg	gtg	tcc	atc	cgg	aag	gct	atg	gac	aac	ttc	cat	432
Lys	Ala	Ala	Ala	Leu	Val	Ser	Ile	Arg	Lys	Ala	Met	Asp	Asn	Phe	His	
130				135				140								
gca	gag	ctc	cat	ccc	cgg	gtg	gcc	ttt	tgg	atc	atg	aag	ctg	cca	cgg	480
Ala	Glu	Leu	His	Pro	Arg	Val	Ala	Phe	Trp	Ile	Met	Lys	Leu	Pro	Arg	
145				150				155				160				
tgg	agg	tcc	cac	cac	aat	gtc	ctg	gag	ggc	ggc	cgc	tgg	ctc	agt	gag	528
Trp	Arg	Ser	His	His	Asn	Val	Leu	Glu	Gly	Gly	Arg	Trp	Leu	Ser	Glu	
165				170				175								
aag	cga	cac	cgc	ctg	cag	gcc	atc	cag	gat	ggg	ctc	cac	gag	ggg	acc	576
Lys	Arg	His	Arg	Leu	Gln	Ala	Ile	Gln	Asp	Gly	Leu	His	Glu	Gly	Thr	
180				185				190								
cgc	gag	gac	gtc	cta	aaa	gag	ggg	acc	cag	ggc	tcc	tcc	cac	tcc	ggg	624
Arg	Glu	Asp	Val	Leu	Lys	Glu	Gly	Thr	Gln	Gly	Ser	Ser	His	Ser	Gly	
195				200				205								
ctg	tcc	tcc	gaa	aga	ccc	act	tac	tgt	aca	tct	tca	ggc	ttt	cct	ggc	672
Leu	Ser	Ser	Glu	Arg	Pro	Thr	Tyr	Cys	Thr	Ser	Ser	Gly	Phe	Pro	Gly	
210				215				220								
agc	tat	agg	ggg	tgg	gac	cgg	gga	gca	cct	gca	agc	tgg	gtt	ggg	gtc	720
Ser	Tyr	Arg	Gly	Trp	Asp	Arg	Gly	Ala	Pro	Ala	Ser	Trp	Val	Gly	Val	
225				230				235				240				
tgg	gtc	agc	gta	tca	aag	ggc	ctg	gca	cat	gga	ccc	aca	ggg	ttg	ggc	768
Trp	Val	Ser	Val	Ser	Lys	Gly	Leu	Ala	His	Gly	Pro	Thr	Gly	Leu	Gly	
245				250				255								
ctg	gag	cct	gga	tcc	agt	ggg	ata	gac	ttt	gtg	aat	gcg	ttc	atg	gag	816
Leu	Glu	Pro	Gly	Ser	Ser	Gly	Ile	Asp	Phe	Val	Asn	Ala	Phe	Met	Glu	

260	265	270	
ggc tac agt aac caa aac atc atg gta cta gta caa aaa cgg ata cat			864
Gly Tyr Ser Asn Gln Asn Ile Met Val Leu Val Gln Lys Arg Ile His			
275	280	285	
aga cca atg caa cag aac aga gag gcc aga aat aag gcc aca cac cta			912
Arg Pro Met Gln Gln Asn Arg Glu Ala Arg Asn Lys Ala Thr His Leu			
290	295	300	
caa cca tct gat ctt cga caa agc tga			939
Gln Pro Ser Asp Leu Arg Gln Ser			
305	310		
<210> 26			
<211> 312			
<212> PRT			
<213> Homo sapiens			
<400> 26			
Met Arg His Pro Leu Val Leu Leu Leu Leu Leu Ser Ala Leu Val Thr			
1	5	10	15
Ser Phe Thr Ala Ala Ser Ile His Asp Ala His Ala Gln Glu Ser Ser			
20	25	30	
Leu Gly Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu			
35	40	45	
Phe Leu Lys Asp Asp Leu Leu Arg Gly Ile Asp Ser Phe Phe Ser Ala			
50	55	60	
Pro Met Asp Phe Arg Gly Leu Pro Arg Asn Tyr Gln Gln Glu Glu Asn			
65	70	75	80
Glu Glu His Gln Leu Arg Asn Asn Thr Leu Ser Ser His Leu His Ile			
85	90	95	
Asp Lys Val Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser Glu Lys			
100	105	110	
Val Val Ala Ser Ile Gln Pro Ala Glu Gly Ser Phe Glu Gly Asn Trp			
115	120	125	
Lys Ala Ala Ala Leu Val Ser Ile Arg Lys Ala Met Asp Asn Phe His			
130	135	140	

Ala Glu Leu His Pro Arg Val Ala Phe Trp Ile Met Lys Leu Pro Arg
145 150 155 160

Trp Arg Ser His His Asn Val Leu Glu Gly Gly Arg Trp Leu Ser Glu
165 170 175

Lys Arg His Arg Leu Gln Ala Ile Gln Asp Gly Leu His Glu Gly Thr
180 185 190

Arg Glu Asp Val Leu Lys Glu Gly Thr Gln Gly Ser Ser His Ser Gly
195 200 205

Leu Ser Ser Glu Arg Pro Thr Tyr Cys Thr Ser Ser Gly Phe Pro Gly
210 215 220

Ser Tyr Arg Gly Trp Asp Arg Gly Ala Pro Ala Ser Trp Val Gly Val
225 230 235 240

Trp Val Ser Val Ser Lys Gly Leu Ala His Gly Pro Thr Gly Leu Gly
245 250 255

Leu Glu Pro Gly Ser Ser Gly Ile Asp Phe Val Asn Ala Phe Met Glu
260 265 270

Gly Tyr Ser Asn Gln Asn Ile Met Val Leu Val Gln Lys Arg Ile His
275 280 285

Arg Pro Met Gln Gln Asn Arg Glu Ala Arg Asn Lys Ala Thr His Leu
290 295 300

Gln Pro Ser Asp Leu Arg Gln Ser
305 310

<210> 27
<211> 1365
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1362)

<400> 27
atg ctg cgg atc ctg tgc ctg gca ctc tgc agc ctg ctg act ggc acg 48
Met Leu Arg Ile Leu Cys Leu Ala Leu Cys Ser Leu Leu Thr Gly Thr
1 5 10 15

cga gct gac cct ggg gca ctg ctg cgg ttg ggc atg gac atc atg aac	96
Arg Ala Asp Pro Gly Ala Leu Leu Arg Leu Gly Met Asp Ile Met Asn	
20 25 30	
cgT gag gtc cag agc gcc atg gat gag agt cat atc ctg gag aag atg	144
Arg Glu Val Gln Ser Ala Met Asp Glu Ser His Ile Leu Glu Lys Met	
35 40 45	
gca gcc gag gca ggc aag aaa cag cca ggg atg aaa cct atc aag ggc	192
Ala Ala Glu Ala Gly Lys Lys Gln Pro Gly Met Lys Pro Ile Lys Gly	
50 55 60	
atc acc aat ttg aag gtg aag gat gtc cag ctg ccc gtc atc aca ctg	240
Ile Thr Asn Leu Lys Val Lys Asp Val Gln Leu Pro Val Ile Thr Leu	
65 70 75 80	
aac ttt gta cct gga gtg ggc atc ttc caa tgt gtg tcc aca ggc atg	288
Asn Phe Val Pro Gly Val Gly Ile Phe Gln Cys Val Ser Thr Gly Met	
85 90 95	
acc gtc act ggc aag agc ttc atg gga ggg aac atg gag atc atc gtg	336
Thr Val Thr Gly Lys Ser Phe Met Gly Gly Asn Met Glu Ile Ile Val	
100 105 110	
gcc ctg aac atc aca gcc acc aac cgg ctt ctg cgg gat gag gag aca	384
Ala Leu Asn Ile Thr Ala Thr Asn Arg Leu Leu Arg Asp Glu Glu Thr	
115 120 125	
ggc ctc ccc gtg ttc aag agt gag ggc tgt gag gtc atc ctg gtc aat	432
Gly Leu Pro Val Phe Lys Ser Glu Gly Cys Glu Val Ile Leu Val Asn	
130 135 140	
gtg aag act aac ctg cct agc aac atg ctc ccc aag atg gtc aac aag	480
Val Lys Thr Asn Leu Pro Ser Asn Met Leu Pro Lys Met Val Asn Lys	
145 150 155 160	
ttc ctg gac agc acc ctg cac aaa gtc ctc cct ggg ctg atg tgt ccc	528
Phe Leu Asp Ser Thr Leu His Lys Val Leu Pro Gly Leu Met Cys Pro	
165 170 175	
gcc atc gat gca gtc ctg gtg tat gtg aac agg aag tgg acc aac ctc	576
Ala Ile Asp Ala Val Leu Val Tyr Val Asn Arg Lys Trp Thr Asn Leu	
180 185 190	
agt gac ccc atg cct gtg ggc cag atg ggc acc gtc aaa tat gtt ctg	624
Ser Asp Pro Met Pro Val Gly Gln Met Gly Thr Val Lys Tyr Val Leu	
195 200 205	

atg tcc gca cca gcc acc aca gcc agc tac atc caa ctg gac ttc agt	672
Met Ser Ala Pro Ala Thr Thr Ala Ser Tyr Ile Gln Leu Asp Phe Ser	
210 215 220	
cct gtg gtg cag cag caa aag ggc aaa acc atc aag ctt gct gat gcc	720
Pro Val Val Gln Gln Gln Lys Gly Lys Thr Ile Lys Leu Ala Asp Ala	
225 230 235 240	
ggg gag gcc ctc acg ttc cct gag ggt tat gcc aaa ggc tcg tcg cag	768
Gly Glu Ala Leu Thr Phe Pro Glu Gly Tyr Ala Lys Gly Ser Ser Gln	
245 250 255	
ctg ctg ctc cca gcc acc ttc ctc tct gca gag ctt gcc ctt ctg cag	816
Leu Leu Leu Pro Ala Thr Phe Leu Ser Ala Glu Leu Ala Leu Leu Gln	
260 265 270	
aag tcc ttt cat gtg aat atc cag gat aca atg att ggt gag ctg ccc	864
Lys Ser Phe His Val Asn Ile Gln Asp Thr Met Ile Gly Glu Leu Pro	
275 280 285	
cca caa acc acc aag acc ctg gct cgc ttc att cct gaa gtg gct gta	912
Pro Gln Thr Thr Lys Thr Leu Ala Arg Phe Ile Pro Glu Val Ala Val	
290 295 300	
gct tat ccc aag tca aag ccc ttg acg acc cag atc aag ata aag aag	960
Ala Tyr Pro Lys Ser Lys Pro Leu Thr Thr Gln Ile Lys Ile Lys Lys	
305 310 315 320	
cct ccc aag gtc act atg aag aca ggc aag agc ctg ctg cac ctc cac	1008
Pro Pro Lys Val Thr Met Lys Thr Gly Lys Ser Leu Leu His Leu His	
325 330 335	
agc acc ctg gag atg ttc gca gct cgg tgg cgg agc aag gct cca atg	1056
Ser Thr Leu Glu Met Phe Ala Ala Arg Trp Arg Ser Lys Ala Pro Met	
340 345 350	
tcc ctc ttt ctc cta gaa gtg cac ttc aat ctg aag gtc cag tac tca	1104
Ser Leu Phe Leu Leu Glu Val His Phe Asn Leu Lys Val Gln Tyr Ser	
355 360 365	
gtg cat gag aac cag ctg cag atg gcc act tct ttg gac aga tta ctg	1152
Val His Glu Asn Gln Leu Gln Met Ala Thr Ser Leu Asp Arg Leu Leu	
370 375 380	
agc ttg tcc cgg aag tcc tca tcg att ggc aac ttc aat gag agg gaa	1200
Ser Leu Ser Arg Lys Ser Ser Ser Ile Gly Asn Phe Asn Glu Arg Glu	
385 390 395 400	

tta act ggc ttc atc acc agc tat ctc gaa gaa gcc tac atc cca gtt 1248
 Leu Thr Gly Phe Ile Thr Ser Tyr Leu Glu Glu Ala Tyr Ile Pro Val
 405 410 415

gtc aat gat gtg ctt caa gtg ggg ctc cca ctc ccg gac ttt ctg gcc 1296
 Val Asn Asp Val Leu Gln Val Gly Leu Pro Leu Pro Asp Phe Leu Ala
 420 425 430

atg aat tac aac ctg gct gag ctg gac ata gta gag ctt ggg ggc atc 1344
 Met Asn Tyr Asn Leu Ala Glu Leu Asp Ile Val Glu Leu Gly Gly Ile
 435 440 445

atg gaa cct gcc gac ata tga 1365
 Met Glu Pro Ala Asp Ile
 450

<210> 28

<211> 454

<212> PRT

<213> Homo sapiens

<400> 28

Met Leu Arg Ile Leu Cys Leu Ala Leu Cys Ser Leu Leu Thr Gly Thr
 1 5 10 15

Arg Ala Asp Pro Gly Ala Leu Leu Arg Leu Gly Met Asp Ile Met Asn
 20 25 30

Arg Glu Val Gln Ser Ala Met Asp Glu Ser His Ile Leu Glu Lys Met
 35 40 45

Ala Ala Glu Ala Gly Lys Lys Gln Pro Gly Met Lys Pro Ile Lys Gly
 50 55 60

Ile Thr Asn Leu Lys Val Lys Asp Val Gln Leu Pro Val Ile Thr Leu
 65 70 75 80

Asn Phe Val Pro Gly Val Gly Ile Phe Gln Cys Val Ser Thr Gly Met
 85 90 95

Thr Val Thr Gly Lys Ser Phe Met Gly Gly Asn Met Glu Ile Ile Val
 100 105 110

Ala Leu Asn Ile Thr Ala Thr Asn Arg Leu Leu Arg Asp Glu Glu Thr
 115 120 125

Gly Leu Pro Val Phe Lys Ser Glu Gly Cys Glu Val Ile Leu Val Asn

130	135	140																	
Val Lys Thr Asn Leu Pro Ser Asn Met Leu Pro Lys Met Val Asn Lys																			
145	150	155	160																
Phe Leu Asp Ser Thr Leu His Lys Val Leu Pro Gly Leu Met Cys Pro																			
	165	170	175																
Ala Ile Asp Ala Val Leu Val Tyr Val Asn Arg Lys Trp Thr Asn Leu																			
	180	185	190																
Ser Asp Pro Met Pro Val Gly Gln Met Gly Thr Val Lys Tyr Val Leu																			
	195	200	205																
Met Ser Ala Pro Ala Thr Thr Ala Ser Tyr Ile Gln Leu Asp Phe Ser																			
	210	215	220																
Pro Val Val Gln Gln Gln Lys Gly Lys Thr Ile Lys Leu Ala Asp Ala																			
	225	230	235	240															
Gly Glu Ala Leu Thr Phe Pro Glu Gly Tyr Ala Lys Gly Ser Ser Gln																			
	245	250	255																
Leu Leu Leu Pro Ala Thr Phe Leu Ser Ala Glu Leu Ala Leu Leu Gln																			
	260	265	270																
Lys Ser Phe His Val Asn Ile Gln Asp Thr Met Ile Gly Glu Leu Pro																			
	275	280	285																
Pro Gln Thr Thr Lys Thr Leu Ala Arg Phe Ile Pro Glu Val Ala Val																			
	290	295	300																
Ala Tyr Pro Lys Ser Lys Pro Leu Thr Thr Gln Ile Lys Ile Lys Lys																			
	305	310	315	320															
Pro Pro Lys Val Thr Met Lys Thr Gly Lys Ser Leu Leu His Leu His																			
	325	330	335																
Ser Thr Leu Glu Met Phe Ala Ala Arg Trp Arg Ser Lys Ala Pro Met																			
	340	345	350																
Ser Leu Phe Leu Leu Glu Val His Phe Asn Leu Lys Val Gln Tyr Ser																			
	355	360	365																
Val His Glu Asn Gln Leu Gln Met Ala Thr Ser Leu Asp Arg Leu Leu																			
	370	375	380																
Ser Leu Ser Arg Lys Ser Ser Ser Ile Gly Asn Phe Asn Glu Arg Glu																			

[illegible]

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<210> 29
<211> 335
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) .. (255)
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<400> 29
atg gga tgc aga ctg ctg acc ctg ctg tgt ttc cta caa cct gct tcc 48
Met Gly Cys Arg Leu Leu Thr Leu Leu Cys Phe Leu Gln Pro Ala Ser
1 5 10 15

agc tcc tcg tgg tct ttg gct ccc aat cca gag ctt tcg cga aca cca 96
Ser Ser Ser Trp Ser Leu Ala Pro Asn Pro Glu Leu Ser Arg Thr Pro
20 25 30

gag ccc ctg tgc ctc tcc ctg cag ctg gct ggg agt tcc agg gca tta 144
Glu Pro Leu Cys Leu Ser Leu Gln Leu Ala Gly Ser Ser Arg Ala Leu
35 40 45

aca cag aca gtc ttt gcc cat cag cca gtg act gta tgg agc ttg gat 192
Thr Gln Thr Val Phe Ala His Gln Pro Val Thr Val Trp Ser Leu Asp
50 55 60

gtg aat aca cag ctc ctg cat ccc tcc gag gca tct cca cac cgt ctc 240
Val Asn Thr Gln Leu Leu His Pro Ser Glu Ala Ser Pro His Arg Leu
65 70 75 80

cca gag aat gtc tgc taaaagctgc tcctcttggg gaggctctgg gctttggaga 295
Pro Glu Asn Val Ser
85

gagcacctgg aattccccac tagaaaagcc caaaaactga

335

<210> 30

<211> 85

<212> PRT

<213> Homo sapiens

<400> 30

Met Gly Cys Arg Leu Leu Thr Leu Leu Cys Phe Leu Gln Pro Ala Ser
1 5 10 15

Ser Ser Ser Trp Ser Leu Ala Pro Asn Pro Glu Leu Ser Arg Thr Pro
20 25 30

Glu Pro Leu Cys Leu Ser Leu Gln Leu Ala Gly Ser Ser Arg Ala Leu
35 40 45

Thr Gln Thr Val Phe Ala His Gln Pro Val Thr Val Trp Ser Leu Asp
50 55 60

Val Asn Thr Gln Leu Leu His Pro Ser Glu Ala Ser Pro His Arg Leu
65 70 75 80

Pro Glu Asn Val Ser
85

<210> 31

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligo primer

<400> 31

ggagaggctc tgaagctaca caa

23

<210> 32

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligo primer

<400> 32
tcagctgcac aagccccctg ct 22

<210> 33
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligo primer

<400> 33
gcagtggttg gagctggaa 19

<210> 34
<211> 228
<212> DNA
<213> Homo sapiens

<400> 34
acccatcttt ttctcttctt cgtgctccta aacttaggt accaagcttt gctggggaaa 60
gcactccagg tgggtgttac tacaaatcac cgtctgctga cccactggta ctacctgaca 120
gcctttgata tttccagagt caatacctgc tttccattct ccacagcatc taatataagt 180
catggcttct catctgtcct gttccccgc ttgcggttca ccactgtg 228

<210> 35
<211> 156
<212> DNA
<213> Homo sapiens

<400> 35
gtgctgagat atagggaaag gaatgggaac aaggaagcca tcgccggcct ctccagctct 60
ggaggcttca cagcttgccct cctccttcgt ctgttgagtc atcccacacg caaccacaac 120
tatgtgggag attctgtgcc aggctttggc aactaa 156

<210> 36
<211> 1772
<212> DNA

<213> Homo sapiens

<400> 36

atgagcccct gaccttgaat atcccctgga gcagaatgcc tccttgcaga acagcaatgc 60
agacagaccc aggagcccag gaaatgagtg agtcgtcctc caccgccgga aatggggcca 120
cgcccgagga gtggccggcc ctggccgaca gccccaccac gtcaccgag gccctgcgga 180
tgatccaccc cattcccgcc gactcctgga gaaacctcat tgaacaaata gggctcctgt 240
atcaggaata ccgagataaa tcgactctcc aagaaatcga aaccaggagg caacaggatg 300
cagaaataga agacaatacc aatgggtccc cgccagtgga ggacaccccg gaggaggaag 360
aagaagagga ggaggaggag gagccggcca gcccaccaga gaggaagact ctgccccaga 420
tctgcctgct cagtaacccc cactcaaggt tcaacctctg gcaggatctt cccgagatcc 480
ggagcagcgg ggtgcttgag atcctacagc ctgaggagat taagctgcag gaggccatgt 540
tcgagctggt cacttccgag gcgtcctact acaagagtct gaacctgctc gtgtcccact 600
tcatggagaa cgagcggata aggaagatcc tgcaccgcgc cgaggcgac atcctcttct 660
ccaacgtcct ggacgtgctg gctgtcagtg agcggttggc cctggagctg gagcaccgga 720
tgaggagaa catggtcatc tctgacgtgt gtgacatcgt gtaccgttat gcggccgacc 780
acttctctgt ctacatcacc tacgtcagca atcagacctt ccaggagcgg acctataagc 840
agctgctcca ggagaaggca gctttccggg agctgatcgc gcagctagag ctcgacccca 900
agtgcagggg gctgcccttc tctccttcc tcatcctgcc ttccagagg atcacacgcc 960
tcaagctggt ggtccagaac atcctgaaga gggtagaaga gaggtctgag cgggagtgca 1020
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ggaaaatgag ccgcacggaa cagatgatca gcattcagaa gaagatggag ttcaagatca 1140
agtcggtgcc catcatctcc cactcccgct ggctgctgaa gcagggtgag ctgcagcaga 1200
tgtcaggccc caagacctcc cggaccctga ggaccaagaa gctcttccac gaaatttacc 1260
tcttctgtt caacgacctg ctggtgatct gccggcagat tccaggagac aagtaccagg 1320
tatttgactc agctccgcgg ggactgctgc gtgtggagga gctggaggac cagggccaga 1380

cgctggccaa cgtgttcac ctcgcggtgc tggagaacgc agatgaccgg gagggccacct 1440
 acatgctaaa ggcgtcctct cagagtgaga tgaagcggtg gatgacctca ctggccccca 1500
 acaggaggac caagtttggt tcgttcacat cccgggtgct ggactgcccc caggtccagt 1560
 gcgtgcaccc atacgtggct cagcagccag acgagctgac gctggagctc gccgacatcc 1620
 tcaacatcct ggacaagact gacgacgggt ggatctttgg cgagcgtctg cagcaccagg 1680
 agagaggctg gttccccagc tccatgactg aggagatctt gaatccaag atccgggtccc 1740
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<210> 37

<211> 511

<212> PRT

<213> Homo sapiens

<400> 37

Arg Arg Cys Ser Lys Leu Ile Asn Ser Ser Gln Leu Leu Tyr Gln Glu
 1 5 10 15

Tyr Ser Asp Val Val Leu Asn Lys Glu Ile Gln Ser Gln Gln Arg Leu
 20 25 30

Glu Ser Leu Ser Glu Thr Pro Gly Pro Ser Ser Pro Arg Gln Pro Arg
 35 40 45

Lys Ala Leu Val Ser Ser Glu Ser Tyr Leu Gln Arg Leu Ser Met Ala
 50 55 60

Ser Ser Gly Ser Leu Trp Gln Glu Ile Pro Val Val Arg Asn Ser Thr
 65 70 75 80

Val Leu Leu Ser Met Thr His Glu Asp Gln Lys Leu Gln Glu Val Lys
 85 90 95

Phe Glu Leu Ile Val Ser Glu Ala Ser Tyr Leu Arg Ser Leu Asn Ile
 100 105 110

Ala Val Asp His Phe Gln Leu Ser Thr Ser Leu Arg Ala Thr Leu Ser
 115 120 125

Asn Gln Glu His Gln Trp Leu Phe Ser Arg Leu Gln Asp Val Arg Asp
 130 135 140

Val	Ser	Ala	Thr	Phe	Leu	Ser	Asp	Leu	Glu	Glu	Asn	Phe	Glu	Asn	Asn	
145					150					155					160	
Ile	Phe	Ser	Phe	Gln	Val	Cys	Asp	Val	Val	Leu	Asn	His	Ala	Pro	Asp	
				165					170						175	
Phe	Arg	Arg	Val	Tyr	Leu	Pro	Tyr	Val	Thr	Asn	Gln	Thr	Tyr	Gln	Glu	
			180					185					190			
Arg	Thr	Phe	Gln	Ser	Leu	Met	Asn	Ser	Asn	Ser	Asn	Phe	Arg	Glu	Val	
		195					200					205				
Leu	Glu	Lys	Leu	Glu	Ser	Asp	Pro	Val	Cys	Gln	Arg	Leu	Ser	Leu	Lys	
	210					215					220					
Ser	Phe	Leu	Ile	Leu	Pro	Phe	Gln	Arg	Ile	Thr	Arg	Leu	Lys	Leu	Leu	
225					230					235					240	
Leu	Gln	Asn	Ile	Leu	Lys	Arg	Thr	Gln	Pro	Gly	Ser	Ser	Glu	Glu	Ala	
				245					250						255	
Glu	Ala	Thr	Lys	Ala	His	His	Ala	Leu	Glu	Gln	Leu	Ile	Arg	Asp	Cys	
			260					265					270			
Asn	Asn	Asn	Val	Gln	Ser	Met	Arg	Arg	Thr	Glu	Glu	Leu	Ile	Tyr	Leu	
		275					280						285			
Ser	Gln	Lys	Ile	Glu	Phe	Glu	Cys	Lys	Ile	Phe	Pro	Leu	Ile	Ser	Gln	
	290					295					300					
Ser	Arg	Trp	Leu	Val	Lys	Ser	Gly	Glu	Leu	Thr	Ala	Leu	Glu	Phe	Ser	
305					310					315					320	
Ala	Ser	Pro	Gly	Leu	Arg	Arg	Lys	Leu	Asn	Thr	Arg	Pro	Val	His	Leu	
				325					330					335		
His	Leu	Phe	Asn	Asp	Cys	Leu	Leu	Leu	Ser	Arg	Pro	Arg	Glu	Gly	Ser	
			340					345					350			
Arg	Phe	Leu	Val	Phe	Asp	His	Ala	Pro	Phe	Ser	Ser	Ile	Arg	Gly	Glu	
		355					360					365				
Lys	Cys	Glu	Met	Lys	Leu	His	Gly	Pro	His	Lys	Asn	Leu	Phe	Arg	Leu	
	370					375					380					
Phe	Leu	Arg	Gln	Asn	Thr	Gln	Gly	Ala	Gln	Ala	Glu	Phe	Leu	Phe	Arg	
385					390					395					400	

Thr Glu Thr Gln Ser Glu Lys Leu Arg Trp Ile Ser Ala Leu Ala Met
405 410 415

Pro Arg Glu Glu Leu Asp Leu Leu Glu Cys Tyr Asn Ser Pro Gln Val
420 425 430

Gln Cys Leu Arg Ala Tyr Lys Pro Arg Glu Asn Asp Glu Leu Ala Leu
435 440 445

Glu Lys Ala Asp Val Val Met Val Thr Gln Gln Ser Ser Asp Gly Trp
450 455 460

Leu Glu Gly Val Arg Leu Ser Asp Gly Glu Arg Gly Trp Phe Pro Val
465 470 475 480

Gln Gln Val Glu Phe Ile Ser Asn Pro Glu Val Arg Ala Gln Asn Leu
485 490 495

Lys Glu Ala His Arg Val Lys Thr Ala Lys Leu Gln Leu Val Glu
500 505 510

<210> 38

<211> 421

<212> PRT

<213> Homo sapiens

<400> 38

Met Phe Glu Ile Leu Thr Ser Glu Phe Ser Tyr Gln His Ser Leu Ser
1 5 10 15

Ile Leu Val Glu Glu Phe Leu Gln Ser Lys Glu Leu Arg Ala Thr Val
20 25 30

Thr Gln Met Glu His His His Leu Phe Ser Asn Ile Leu Asp Val Leu
35 40 45

Gly Ala Ser Gln Arg Phe Phe Glu Asp Leu Glu Gln Arg His Lys Ala
50 55 60

Gln Val Leu Val Glu Asp Ile Ser Asp Ile Leu Glu Glu His Ala Glu
65 70 75 80

Lys Tyr Phe His Pro Tyr Ile Ala Tyr Cys Ser Asn Glu Val Tyr Gln
85 90 95

Gln Arg Thr Leu Gln Lys Leu Ile Ser Ser Asn Ala Ala Phe Arg Glu

100	105	110
Ala Leu Arg Glu Ile Glu Arg Arg Pro Ala Cys Gly Gly Leu Pro Met		
115	120	125
Leu Ser Phe Leu Ile Leu Pro Met Gln Arg Val Thr Arg Leu Pro Leu		
130	135	140
Leu Met Asp Thr Leu Cys Leu Lys Thr Gln Gly His Ser Glu Arg Tyr		
145	150	155
Lys Ala Ala Ser Arg Ala Leu Lys Ala Ile Ser Lys Leu Val Arg Gln		
165	170	175
Cys Asn Glu Gly Ala His Arg Met Glu Arg Met Glu Gln Met Tyr Thr		
180	185	190
Leu His Thr Gln Leu Asp Phe Ser Lys Val Lys Ser Leu Pro Leu Ile		
195	200	205
Ser Ala Ser Arg Trp Leu Leu Lys Arg Gly Glu Leu Phe Leu Val Glu		
210	215	220
Glu Thr Gly Leu Phe Arg Lys Ile Ala Ser Arg Pro Thr Cys Tyr Leu		
225	230	235
Phe Leu Phe Asn Asp Val Leu Val Val Thr Lys Lys Lys Ser Glu Glu		
245	250	255
Ser Tyr Met Val Gln Asp Tyr Ala Gln Met Asn His Ile Gln Val Glu		
260	265	270
Lys Ile Glu Pro Ser Glu Leu Pro Leu Pro Gly Gly Gly Asn Arg Ser		
275	280	285
Ser Ser Val Pro His Pro Phe Gln Val Thr Leu Leu Arg Asn Ser Glu		
290	295	300
Gly Arg Gln Glu Gln Leu Leu Leu Ser Ser Asp Ser Ala Ser Asp Arg		
305	310	315
Ala Arg Trp Ile Val Ala Leu Thr His Ser Glu Arg Gln Trp Gln Gly		
325	330	335
Leu Ser Ser Lys Gly Asp Leu Pro Gln Val Glu Ile Thr Lys Ala Phe		
340	345	350
Phe Ala Lys Gln Ala Asp Glu Val Thr Leu Gln Gln Ala Asp Val Val		

Ser	Leu	Asn	Ile	Ala	Val	Asp	His	Phe	Gln	Leu	Ser	Thr	Ser	Leu	Arg	145	150	155	160
Ala	Thr	Leu	Ser	Asn	Gln	Glu	His	Gln	Trp	Leu	Phe	Ser	Arg	Leu	Gln	165	170	175	
Asp	Val	Arg	Asp	Val	Ser	Ala	Thr	Phe	Leu	Ser	Asp	Leu	Glu	Glu	Asn	180	185	190	
Phe	Glu	Asn	Asn	Ile	Phe	Ser	Phe	Gln	Val	Cys	Asp	Val	Val	Leu	Asn	195	200	205	
His	Ala	Pro	Asp	Phe	Arg	Arg	Val	Tyr	Leu	Pro	Tyr	Val	Thr	Asn	Gln	210	215	220	
Thr	Tyr	Gln	Glu	Arg	Thr	Phe	Gln	Ser	Leu	Met	Asn	Ser	Asn	Ser	Asn	225	230	235	240
Phe	Arg	Glu	Val	Leu	Glu	Lys	Leu	Glu	Ser	Asp	Pro	Val	Cys	Gln	Arg	245	250	255	
Leu	Ser	Leu	Lys	Ser	Phe	Leu	Ile	Leu	Pro	Phe	Gln	Arg	Ile	Thr	Arg	260	265	270	
Leu	Lys	Leu	Leu	Leu	Gln	Asn	Ile	Leu	Lys	Arg	Thr	Gln	Pro	Gly	Ser	275	280	285	
Ser	Glu	Glu	Ala	Glu	Ala	Thr	Lys	Ala	His	His	Ala	Leu	Glu	Gln	Leu	290	295	300	
Ile	Arg	Asp	Cys	Asn	Asn	Asn	Val	Gln	Ser	Met	Arg	Arg	Thr	Glu	Glu	305	310	315	320
Leu	Ile	Tyr	Leu	Ser	Gln	Lys	Ile	Glu	Phe	Glu	Cys	Lys	Ile	Phe	Pro	325	330	335	
Leu	Ile	Ser	Gln	Ser	Arg	Trp	Leu	Val	Lys	Ser	Gly	Glu	Leu	Thr	Ala	340	345	350	
Leu	Glu	Phe	Ser	Ala	Ser	Pro	Gly	Leu	Arg	Arg	Lys	Leu	Asn	Thr	Arg	355	360	365	
Pro	Val	His	Leu	His	Leu	Phe	Asn	Asp	Cys	Leu	Leu	Leu	Ser	Arg	Pro	370	375	380	
Arg	Glu	Gly	Ser	Arg	Phe	Leu	Val	Phe	Asp	His	Ala	Pro	Phe	Ser	Ser	385	390	395	400

Ile Arg Gly Glu Lys Cys Glu Met Lys Leu His Gly Pro His Lys Asn
 405 410 415

Leu Phe Arg Leu Phe Leu Arg Gln Asn Thr Gln Gly Ala Gln Ala Glu
 420 425 430

Phe Leu Phe Arg Thr Glu Thr Gln Ser Glu Lys Leu Arg Trp Ile Ser
 435 440 445

Ala Leu Ala Met Pro Arg Glu Glu Leu Asp Leu Leu Glu Cys Tyr Asn
 450 455 460

Ser Pro Gln Val Gln Cys Leu Arg Ala Tyr Lys Pro Arg Glu Asn Asp
 465 470 475 480

Glu Leu Ala Leu Glu Lys Ala Asp Val Val Met Val Thr Gln Gln Ser
 485 490 495

Ser Asp Gly Trp Leu Glu Gly Val Arg Leu Ser Asp Gly Glu Arg Gly
 500 505 510

Trp Phe Pro Val Gln Gln Val Glu Phe Ile Ser Asn Pro Glu Val Arg
 515 520 525

Ala Gln Asn Leu Lys Glu Ala His Arg Val Lys Thr Ala Lys Leu Gln
 530 535 540

Leu Val Glu Gln Gln Ala
 545 550

<210> 40
 <211> 519
 <212> PRT
 <213> Homo sapiens

<400> 40
 Met Gly Gly Phe Ser Arg Arg Cys Ser Lys Leu Ile Asn Ser Ser Gln
 1 5 10 15

Leu Leu Tyr Gln Glu Tyr Ser Asp Val Val Leu Asn Lys Glu Ile Gln
 20 25 30

Ser Gln Gln Arg Leu Glu Ser Leu Ser Glu Thr Pro Gly Pro Ser Ser
 35 40 45

Pro Arg Gln Pro Arg Lys Ala Leu Val Ser Ser Glu Ser Tyr Leu Gln
 50 55 60

Arg	Leu	Ser	Met	Ala	Ser	Ser	Gly	Ser	Leu	Trp	Gln	Glu	Ile	Pro	Val	65	70	75	80
Val	Arg	Asn	Ser	Thr	Val	Leu	Leu	Ser	Met	Thr	His	Glu	Asp	Gln	Lys	85	90	95	
Leu	Gln	Glu	Val	Lys	Phe	Glu	Leu	Ile	Val	Ser	Glu	Ala	Ser	Tyr	Leu	100	105	110	
Arg	Ser	Leu	Asn	Ile	Ala	Val	Asp	His	Phe	Gln	Leu	Ser	Thr	Ser	Leu	115	120	125	
Arg	Ala	Thr	Leu	Ser	Asn	Gln	Glu	His	Gln	Trp	Leu	Phe	Ser	Arg	Leu	130	135	140	
Gln	Asp	Val	Arg	Asp	Val	Ser	Ala	Thr	Phe	Leu	Ser	Asp	Leu	Glu	Glu	145	150	155	160
Asn	Phe	Glu	Asn	Asn	Ile	Phe	Ser	Phe	Gln	Val	Cys	Asp	Val	Val	Leu	165	170	175	
Asn	His	Ala	Pro	Asp	Phe	Arg	Arg	Val	Tyr	Leu	Pro	Tyr	Val	Thr	Asn	180	185	190	
Gln	Thr	Tyr	Gln	Glu	Arg	Thr	Phe	Gln	Ser	Leu	Met	Asn	Ser	Asn	Ser	195	200	205	
Asn	Phe	Arg	Glu	Val	Leu	Glu	Lys	Leu	Glu	Ser	Asp	Pro	Val	Cys	Gln	210	215	220	
Arg	Leu	Ser	Leu	Lys	Ser	Phe	Leu	Ile	Leu	Pro	Phe	Gln	Arg	Ile	Thr	225	230	235	240
Arg	Leu	Lys	Leu	Leu	Leu	Gln	Asn	Ile	Leu	Lys	Arg	Thr	Gln	Pro	Gly	245	250	255	
Ser	Ser	Glu	Glu	Ala	Glu	Ala	Thr	Lys	Ala	His	His	Ala	Leu	Glu	Gln	260	265	270	
Leu	Ile	Arg	Asp	Cys	Asn	Asn	Asn	Val	Gln	Ser	Met	Arg	Arg	Thr	Glu	275	280	285	
Glu	Leu	Ile	Tyr	Leu	Ser	Gln	Lys	Ile	Glu	Phe	Glu	Cys	Lys	Ile	Phe	290	295	300	
Pro	Leu	Ile	Ser	Gln	Ser	Arg	Trp	Leu	Val	Lys	Ser	Gly	Glu	Leu	Thr	305	310	315	320

Ala Leu Glu Phe Ser Ala Ser Pro Gly Leu Arg Arg Lys Leu Asn Thr
325 330 335

Arg Pro Val His Leu His Leu Phe Asn Asp Cys Leu Leu Leu Ser Arg
340 345 350

Pro Arg Glu Gly Ser Arg Phe Leu Val Phe Asp His Ala Pro Phe Ser
355 360 365

Ser Ile Arg Gly Glu Lys Cys Glu Met Lys Leu His Gly Pro His Lys
370 375 380

Asn Leu Phe Arg Leu Phe Leu Arg Gln Asn Thr Gln Gly Ala Gln Ala
385 390 395 400

Glu Phe Leu Phe Arg Thr Glu Thr Gln Ser Glu Lys Leu Arg Trp Ile
405 410 415

Ser Ala Leu Ala Met Pro Arg Glu Glu Leu Asp Leu Leu Glu Cys Tyr
420 425 430

Asn Ser Pro Gln Val Gln Cys Leu Arg Ala Tyr Lys Pro Arg Glu Asn
435 440 445

Asp Glu Leu Ala Leu Glu Lys Ala Asp Val Val Met Val Thr Gln Gln
450 455 460

Ser Ser Asp Gly Trp Leu Glu Gly Val Arg Leu Ser Asp Gly Glu Arg
465 470 475 480

Gly Trp Phe Pro Val Gln Gln Val Glu Phe Ile Ser Asn Pro Glu Val
485 490 495

Arg Ala Gln Asn Leu Lys Glu Ala His Arg Val Lys Thr Ala Lys Leu
500 505 510

Gln Leu Val Glu Gln Gln Ala
515

<210> 41

<211> 554

<212> PRT

<213> Mus musculus

<400> 41

Met Ile His Pro Ile Pro Ala Asp Ser Trp Arg Asn Leu Ile Glu Gln

1	5	10	15
Ile Gly Leu Leu Tyr Gln Glu Tyr Arg Asp Lys Ser Thr Leu Gln Glu	20	25	30
Ile Glu Thr Arg Arg Gln Gln Asp Ala Glu Ile Gln Gly Asn Ser Asp	35	40	45
Gly Ser Gln Val Gly Glu Asp Ala Gly Glu Glu Glu Glu Glu Glu Glu	50	55	60
Glu Gly Glu Glu Glu Glu Leu Ala Ser Pro Pro Glu Arg Arg Ala Leu	65	70	75
Pro Gln Ile Cys Leu Leu Ser Asn Pro His Ser Arg Phe Asn Leu Trp	85	90	95
Gln Asp Leu Pro Glu Ile Gln Ser Ser Gly Val Leu Asp Ile Leu Gln	100	105	110
Pro Glu Glu Ile Arg Leu Gln Glu Ala Met Phe Glu Leu Val Thr Ser	115	120	125
Glu Ala Ser Tyr Tyr Lys Ser Leu Asn Leu Leu Val Ser His Phe Met	130	135	140
Glu Asn Glu Arg Leu Lys Lys Ile Leu His Pro Ser Glu Ala His Ile	145	150	155
Leu Phe Ser Asn Val Leu Asp Val Met Ala Val Ser Glu Arg Phe Leu	165	170	175
Leu Glu Leu Glu His Arg Met Glu Glu Asn Ile Val Ile Ser Asp Val	180	185	190
Cys Asp Ile Val Tyr Arg Tyr Ala Ala Asp His Phe Ser Val Tyr Ile	195	200	205
Thr Tyr Val Ser Asn Gln Thr Tyr Gln Glu Arg Thr Tyr Lys Gln Leu	210	215	220
Leu Gln Glu Lys Ala Ala Phe Arg Glu Leu Ile Ala Gln Leu Glu Leu	225	230	235
Asp Pro Lys Cys Lys Gly Leu Pro Phe Ser Ser Phe Leu Ile Leu Pro	245	250	255
Phe Gln Arg Ile Thr Arg Leu Lys Leu Leu Val Gln Asn Ile Leu Lys			

260	265	270
Arg Val Glu Glu Arg Ser Glu Arg Glu Gly Thr Ala Leu Asp Ala His		
275	280	285
Lys Glu Leu Glu Met Val Val Lys Ala Cys Asn Glu Gly Val Arg Lys		
290	295	300
Met Ser Arg Thr Glu Gln Met Ile Ser Ile Gln Lys Lys Met Glu Phe		
305	310	315
Lys Ile Lys Ser Val Pro Ile Ile Ser His Ser Arg Trp Leu Leu Lys		
325	330	335
Gln Gly Glu Leu Gln Gln Met Ser Gly Pro Lys Thr Ser Arg Thr Leu		
340	345	350
Arg Thr Lys Lys Leu Phe Arg Glu Ile Tyr Leu Phe Leu Phe Asn Asp		
355	360	365
Leu Leu Val Ile Cys Arg Gln Ile Pro Gly Asp Lys Tyr Gln Val Phe		
370	375	380
Asp Ser Ala Pro Arg Gly Leu Leu Arg Val Glu Glu Leu Glu Asp Gln		
385	390	395
Gly Gln Thr Leu Ala Asn Val Phe Ile Leu Arg Leu Leu Glu Asn Ala		
405	410	415
Asp Asp Arg Glu Ala Thr Tyr Met Leu Lys Ala Ser Ser Gln Ser Glu		
420	425	430
Met Lys Arg Trp Met Thr Ser Leu Ala Pro Asn Arg Arg Thr Lys Phe		
435	440	445
Val Ser Phe Thr Ser Arg Leu Leu Asp Cys Pro Gln Val Gln Cys Val		
450	455	460
His Pro Tyr Val Ala Gln Gln Pro Asp Glu Leu Thr Leu Glu Leu Ala		
465	470	475
Asp Ile Leu Asn Ile Leu Glu Lys Thr Glu Asp Gly Trp Ile Phe Gly		
485	490	495
Glu Arg Leu His Asp Gln Glu Arg Gly Trp Phe Pro Ser Ser Met Thr		
500	505	510
Glu Glu Ile Leu Asn Pro Lys Ile Arg Ser Gln Asn Leu Lys Glu Cys		

515

520

525

Phe Arg Val His Lys Met Glu Asp Pro Gln Arg Ser Gln Asn Lys Asp
530 535 540

Arg Arg Lys Leu Gly Ser Arg Asn Arg Gln
545 550

<210> 42

<211> 381

<212> DNA

<213> Homo sapiens

<400> 42

tcccaagtat gaactgatca tcgaggctca agatatggct ggactggatg ttggattaac 60
aggcacggcc acagccacga tcatgatcga tgacaaaaat gatcactcac caaaattcac 120
caagaaagag tttcaagcca cagtcgagga aggagctgtg ggagttattg tcaatttgac 180
agttgaagat aaggatgacc ccaccacagg tgcattggagg gctgcctaca ccatcatcaa 240
cggaaacccc gggcagagct ttgaaatcca caccaaccct caaaccaacg aagggatgct 300
ttctgttgtc aaaccattgg actatgaaat ttctgccttc cacaccctgc tgatcaaagt 360
ggaaaatgaa gaccactcg t 381

<210> 43

<211> 413

<212> PRT

<213> Homo sapiens

<400> 43

Gly Asn Gln Val Glu Asn Pro Ile Asp Ile Val Ile Asn Val Ile Asp
1 5 10 15
Met Asn Asp Asn Arg Pro Glu Phe Leu His Gln Val Trp Asn Gly Thr
20 25 30
Val Pro Glu Gly Ser Lys Pro Gly Thr Tyr Val Met Thr Val Thr Ala
35 40 45
Ile Asp Ala Asp Asp Pro Asn Ala Leu Asn Gly Met Leu Arg Tyr Arg
50 55 60

Ile Val Ser Gln Ala Pro Ser Thr Pro Ser Pro Asn Met Phe Thr Ile	65	70	75	80
Asn Asn Glu Thr Gly Asp Ile Ile Thr Val Ala Ala Gly Leu Asp Arg	85	90	95	
Glu Lys Val Gln Gln Tyr Thr Leu Ile Ile Gln Ala Thr Asp Met Glu	100	105	110	
Gly Asn Pro Thr Tyr Gly Leu Ser Asn Thr Ala Thr Ala Val Ile Thr	115	120	125	
Val Thr Asp Val Asn Asp Asn Pro Pro Glu Phe Thr Ala Met Thr Phe	130	135	140	
Tyr Gly Glu Val Pro Glu Asn Arg Val Asp Ile Ile Val Ala Asn Leu	145	150	155	160
Thr Val Thr Asp Lys Asp Gln Pro His Thr Pro Ala Trp Asn Ala Val	165	170	175	
Tyr Arg Ile Ser Gly Gly Asp Pro Thr Gly Arg Phe Ala Ile Gln Thr	180	185	190	
Asp Pro Asn Ser Asn Asp Gly Leu Val Thr Val Val Lys Pro Ile Asp	195	200	205	
Phe Glu Thr Asn Arg Met Phe Val Leu Thr Val Ala Ala Glu Asn Gln	210	215	220	
Val Pro Leu Ala Lys Gly Ile Gln His Pro Pro Gln Ser Thr Ala Thr	225	230	235	240
Val Ser Val Thr Val Ile Asp Val Asn Glu Asn Pro Tyr Phe Ala Pro	245	250	255	
Asn Pro Lys Ile Ile Arg Gln Glu Glu Gly Leu His Ala Gly Thr Met	260	265	270	
Leu Thr Thr Phe Thr Ala Gln Asp Pro Asp Arg Tyr Met Gln Gln Asn	275	280	285	
Ile Arg Tyr Thr Lys Leu Ser Asp Pro Ala Asn Trp Leu Lys Ile Asp	290	295	300	
Pro Val Asn Gly Gln Ile Thr Thr Ile Ala Val Leu Asp Arg Glu Ser	305	310	315	320

Pro Asn Val Lys Asn Asn Ile Tyr Asn Ala Thr Phe Leu Ala Ser Asp
 325 330 335
 Asn Gly Ile Pro Pro Met Ser Gly Thr Gly Thr Leu Gln Ile Tyr Leu
 340 345 350
 Leu Asp Ile Asn Asp Asn Ala Pro Gln Val Leu Pro Gln Glu Ala Glu
 355 360 365
 Thr Cys Glu Thr Pro Asp Pro Asn Ser Ile Asn Ile Thr Ala Leu Asp
 370 375 380
 Tyr Asp Ile Asp Pro Asn Ala Gly Pro Phe Ala Phe Asp Leu Pro Leu
 385 390 395 400
 Ser Pro Val Thr Ile Lys Arg Asn Trp Thr Ile Thr Arg
 405 410

<210> 44

<211> 80

<212> PRT

<213> Homo sapiens

<400> 44

Leu Gln Arg Gln Lys Arg Asp Trp Val Ile Pro Pro Ile Asn Leu Pro
 1 5 10 15

Glu Asn Ser Arg Gly Pro Phe Pro Gln Glu Leu Val Arg Ile Arg Ser
 20 25 30

Asp Arg Asp Lys Asn Leu Ser Leu Arg Tyr Ser Val Thr Gly Pro Gly
 35 40 45

Ala Asp Gln Pro Pro Thr Gly Ile Phe Ile Ile Asn Pro Ile Ser Gly
 50 55 60

Gln Leu Ser Val Thr Lys Pro Leu Asp Arg Glu Gln Ile Ala Arg Phe
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<210> 45

<211> 905

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (92)

<223> Wherein N may be a or t or g or c

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atgaactggg tcatgaccca gcaaattggg tnagcgtcga caaaaactcc ggagtgggtca 120
tcaccgtgga gccaatggac cgagaatccc ctcatgtaaa taacagtttt tatgtaatca 180
tcattcacgc tgttgatgat ggcttcccac cgcagactgc tacagggacc ctaatgctct 240
tctgtctga catcaatgac aacgtcccga ctctccggcc acgttcccgc tacatggagg 300
tctgtgagtc tgctgtgcat gagccccctc acatcgaggc agaggatccg gacctggagc 360
cgttctctga cccatttaca tttgaattgg acaatacctg gggaaatgag gaggacacat 420
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cagtggctct gctttttctg ttgcatgct attttgtgct tgaacctaa aggcattggat 720
gctctgtatc caatgatgaa ggccacaaa cactggatcat gtataatgag gagagcaaag 780
gcatttcagc ccagacatgg tcagatgttg aaggccagag gccggctctg ctcatctgca 840
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aactc 905
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<210> 46

<211> 906

<212> PRT

<213> Homo sapiens

<400> 46

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Met Cys Arg Ile Ala Gly Ala Leu Arg Thr Leu Leu Pro Leu Leu Leu
  1           5           10          15
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Ala	Leu	Leu	Gln	Ala	Ser	Val	Glu	Ala	Ser	Gly	Glu	Ile	Ala	Leu	Cys	20	25	30	
Lys	Thr	Gly	Phe	Pro	Glu	Asp	Val	Tyr	Ser	Ala	Val	Leu	Ser	Lys	Asp	35	40	45	
Val	His	Glu	Gly	Gln	Pro	Leu	Leu	Asn	Val	Lys	Phe	Ser	Asn	Cys	Asn	50	55	60	
Gly	Lys	Arg	Lys	Val	Gln	Tyr	Glu	Ser	Ser	Glu	Pro	Ala	Asp	Phe	Lys	65	70	75	80
Val	Asp	Glu	Asp	Gly	Met	Val	Tyr	Ala	Val	Arg	Ser	Phe	Pro	Leu	Ser	85	90	95	
Ser	Glu	His	Ala	Lys	Phe	Leu	Ile	Val	Ala	Gln	Asp	Lys	Glu	Thr	Gln	100	105	110	
Glu	Lys	Trp	Gln	Val	Ala	Val	Lys	Leu	Ser	Leu	Lys	Pro	Thr	Leu	Thr	115	120	125	
Glu	Glu	Ser	Val	Lys	Glu	Ser	Ala	Glu	Val	Glu	Glu	Ile	Val	Phe	Pro	130	135	140	
Arg	Gln	Phe	Ser	Lys	His	Ser	Gly	His	Leu	Gln	Arg	Gln	Lys	Arg	Asp	145	150	155	160
Trp	Val	Ile	Pro	Pro	Ile	Asn	Leu	Pro	Glu	Asn	Ser	Arg	Gly	Pro	Phe	165	170	175	
Pro	Gln	Glu	Leu	Val	Arg	Ile	Arg	Ser	Asp	Arg	Asp	Lys	Asn	Leu	Ser	180	185	190	
Leu	Arg	Tyr	Ser	Val	Thr	Gly	Pro	Gly	Ala	Asp	Gln	Pro	Pro	Thr	Gly	195	200	205	
Ile	Phe	Ile	Ile	Asn	Pro	Ile	Ser	Gly	Gln	Leu	Ser	Val	Thr	Lys	Pro	210	215	220	
Leu	Asp	Arg	Glu	Gln	Ile	Ala	Arg	Phe	His	Leu	Arg	Ala	His	Ala	Val	225	230	235	240
Asp	Ile	Asn	Gly	Asn	Gln	Val	Glu	Asn	Pro	Ile	Asp	Ile	Val	Ile	Asn	245	250	255	
Val	Ile	Asp	Met	Asn	Asp	Asn	Arg	Pro	Glu	Phe	Leu	His	Gln	Val	Trp	260	265	270	

Asn Gly Thr Val Pro Glu Gly Ser Lys Pro Gly Thr Tyr Val Met Thr	275	280	285
Val Thr Ala Ile Asp Ala Asp Asp Pro Asn Ala Leu Asn Gly Met Leu	290	295	300
Arg Tyr Arg Ile Val Ser Gln Ala Pro Ser Thr Pro Ser Pro Asn Met	305	310	315 320
Phe Thr Ile Asn Asn Glu Thr Gly Asp Ile Ile Thr Val Ala Ala Gly	325	330	335
Leu Asp Arg Glu Lys Val Gln Gln Tyr Thr Leu Ile Ile Gln Ala Thr	340	345	350
Asp Met Glu Gly Asn Pro Thr Tyr Gly Leu Ser Asn Thr Ala Thr Ala	355	360	365
Val Ile Thr Val Thr Asp Trp Asn Asp Asn Pro Pro Glu Glu Thr Ala	370	375	380
Met Thr Phe Tyr Gly Glu Val Pro Glu Asn Arg Val Asp Ile Ile Val	385	390	395 400
Ala Asn Leu Thr Val Thr Asp Lys Asp Gln Pro His Thr Pro Ala Trp	405	410	415
Asn Ala Val Tyr Arg Ile Ser Gly Gly Asp Pro Thr Gly Arg Phe Ala	420	425	430
Ile Gln Thr Asp Pro Asn Ser Asn Asp Gly Leu Val Thr Val Val Lys	435	440	445
Pro Ile Asp Phe Glu Thr Asn Arg Met Phe Val Leu Thr Val Ala Ala	450	455	460
Glu Asn Gln Val Pro Leu Ala Lys Gly Ile Gln His Pro Pro Gln Ser	465	470	475 480
Thr Ala Thr Val Ser Val Thr Val Ile Asp Val Asn Glu Asn Pro Tyr	485	490	495
Phe Ala Pro Asn Pro Lys Ile Ile Arg Gln Glu Glu Gly Leu His Ala	500	505	510
Gly Thr Met Leu Thr Thr Phe Thr Ala Gln Asp Pro Asp Arg Tyr Met	515	520	525

Gln Gln Asn Ile Arg Tyr Thr Lys Leu Ser Asp Pro Ala Asn Trp Leu			
530	535	540	
Lys Ile Asp Pro Val Asn Gly Gln Ile Thr Thr Ile Ala Val Leu Asp			
545	550	555	560
Arg Glu Ser Pro Asn Val Lys Asn Asn Ile Tyr Asn Ala Thr Phe Leu			
	565	570	575
Ala Ser Asp Asn Gly Ile Pro Pro Met Ser Gly Thr Gly Thr Leu Gln			
	580	585	590
Ile Tyr Leu Leu Asp Ile Asn Asp Asn Ala Pro Gln Val Leu Pro Gln			
	595	600	605
Glu Ala Glu Thr Cys Glu Thr Pro Asp Pro Asn Ser Ile Asn Ile Thr			
	610	615	620
Ala Leu Asp Tyr Asp Ile Asp Pro Asn Ala Gly Pro Phe Ala Phe Asp			
625	630	635	640
Leu Pro Leu Ser Pro Val Thr Ile Lys Arg Asn Trp Thr Ile Thr Arg			
	645	650	655
Leu Asn Gly Asp Phe Ala Gln Leu Asn Leu Lys Ile Lys Phe Leu Glu			
	660	665	670
Ala Gly Ile Tyr Glu Val Pro Ile Ile Ile Thr Asp Ser Gly Asn Pro			
	675	680	685
Pro Lys Ser Asn Ile Ser Ile Leu Arg Val Lys Val Cys Gln Cys Asp			
	690	695	700
Ser Asn Gly Asp Cys Thr Asp Val Asp Arg Ile Val Gly Ala Gly Leu			
705	710	715	720
Gly Thr Gly Ala Ile Ile Ala Ile Leu Leu Cys Ile Ile Ile Leu Leu			
	725	730	735
Ile Leu Val Leu Met Phe Val Val Trp Met Lys Arg Arg Asp Lys Glu			
	740	745	750
Arg Gln Ala Lys Gln Leu Leu Ile Asp Pro Glu Asp Asp Val Arg Asp			
	755	760	765
Asn Ile Leu Lys Tyr Asp Glu Glu Gly Gly Gly Glu Glu Asp Gln Asp			
	770	775	780

09746491-074301
T06T40 T06T40

Tyr	Asp	Leu	Ser	Gln	Leu	Gln	Gln	Pro	Asp	Thr	Val	Glu	Pro	Asp	Ala	
785					790					795					800	
Ile	Lys	Pro	Val	Gly	Ile	Arg	Arg	Met	Asp	Glu	Arg	Pro	Ile	His	Ala	
				805					810					815		
Glu	Pro	Gln	Tyr	Pro	Val	Arg	Ser	Ala	Ala	Pro	His	Pro	Gly	Asp	Ile	
			820					825					830			
Gly	Asp	Phe	Ile	Asn	Glu	Gly	Leu	Lys	Ala	Ala	Asp	Asn	Asp	Pro	Thr	
	835						840					845				
Ala	Pro	Pro	Tyr	Asp	Ser	Leu	Leu	Val	Phe	Asp	Tyr	Glu	Gly	Ser	Gly	
	850					855					860					
Ser	Thr	Ala	Gly	Ser	Leu	Ser	Ser	Leu	Asn	Ser	Ser	Ser	Ser	Gly	Gly	
865					870					875				880		
Glu	Gln	Asp	Tyr	Asp	Tyr	Leu	Asn	Asp	Trp	Gly	Pro	Arg	Phe	Lys	Lys	
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Leu	Ala	Asp	Met	Tyr	Gly	Gly	Gly	Asp	Asp							
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Ser	Arg	Asp	Val	Leu	Glu	Gly	Gln	Pro	Leu	Leu	Asn	Val	Lys	Phe	Ser	
			20					25					30			
Asn	Cys	Asn	Gly	Lys	Arg	Lys	Val	Gln	Tyr	Glu	Ser	Ser	Glu	Pro	Ala	
		35					40					45				
Asp	Phe	Lys	Val	Asp	Glu	Asp	Gly	Met	Val	Tyr	Ala	Val	Arg	Ser	Phe	
	50					55					60					
Pro	Leu	Ser	Ser	Glu	His	Ser	Lys	Phe	Leu	Ile	Tyr	Ala	Gln	Asp	Lys	
65					70					75				80		
Glu	Thr	Gln	Glu	Lys	Trp	Gln	Val	Ala	Val	Lys	Leu	Ser	Leu	Lys	Pro	

				85					90					95	
Ala	Leu	Pro	Glu	Asp	Ser	Val	Lys	Glu	Ser	Arg	Glu	Ile	Glu	Glu	Ile
			100					105					110		
Val	Phe	Pro	Arg	Gln	Val	Thr	Lys	His	Asn	Gly	Tyr	Leu	Gln	Arg	Gln
		115					120					125			
Lys	Arg	Asp	Trp	Val	Ile	Pro	Pro	Ile	Asn	Leu	Pro	Glu	Asn	Ser	Arg
	130					135					140				
Gly	Pro	Phe	Pro	Gln	Glu	Leu	Val	Arg	Ile	Arg	Ser	Asp	Arg	Asp	Lys
145					150					155					160
Asn	Leu	Ser	Leu	Arg	Tyr	Ser	Val	Thr	Gly	Pro	Gly	Ala	Asp	Gln	Pro
				165					170					175	
Pro	Thr	Gly	Ile	Phe	Ile	Ile	Asn	Pro	Ile	Ser	Gly	Gln	Leu	Ser	Val
			180					185					190		
Thr	Lys	Pro	Leu	Asp	Arg	Glu	Leu	Ile	Ala	Arg	Phe	His	Leu	Arg	Ala
		195					200					205			
His	Ala	Val	Asp	Ile	Asn	Gly	Asn	Gln	Val	Glu	Asn	Pro	Ile	Asp	Ile
	210					215					220				
Val	Ile	Asn	Val	Ile	Asp	Met	Asn	Asp	Asn	Arg	Pro	Glu	Phe	Leu	His
225					230					235					240
Gln	Val	Trp	Asn	Gly	Thr	Val	Pro	Glu	Gly	Ser	Lys	Pro	Gly	Thr	Tyr
				245					250					255	
Val	Met	Thr	Val	Thr	Ala	Ile	Asp	Ala	Asp	Asp	Pro	Asn	Ala	Leu	Asn
			260					265					270		
Gly	Met	Leu	Arg	Tyr	Arg	Ile	Leu	Ser	Gln	Ala	Pro	Ser	Thr	Pro	Ser
		275					280					285			
Pro	Asn	Met	Phe	Thr	Ile	Asn	Asn	Glu	Thr	Gly	Asp	Ile	Ile	Thr	Val
	290					295					300				
Ala	Ala	Gly	Leu	Asp	Arg	Glu	Lys	Val	Gln	Gln	Tyr	Thr	Leu	Ile	Ile
305					310					315					320
Gln	Ala	Thr	Asp	Met	Glu	Gly	Asn	Pro	Thr	Tyr	Gly	Leu	Ser	Asn	Thr
				325					330					335	
Ala	Thr	Ala	Val	Ile	Thr	Val	Thr	Asp	Trp	Asn	Asp	Asn	Pro	Pro	Glu

340	345	350
Glu Thr Ala Met Thr Phe Tyr Gly Glu Val Pro Glu Asn Arg Val Asp		
355	360	365
Val Ile Val Ala Asn Leu Thr Val Thr Asp Lys Asp Gln Pro His Thr		
370	375	380
Pro Ala Trp Asn Ala Ile Tyr Arg Ile Ser Gly Gly Asp Pro Ala Gly		
385	390	395
Arg Phe Ala Ile Gln Thr Asp Pro Asn Ser Asn Asp Gly Leu Val Thr		
405	410	415
Val Val Lys Pro Ile Asp Phe Glu Thr Asn Arg Met Tyr Val Leu Thr		
420	425	430
Val Ala Ala Glu Asn Gln Val Pro Leu Ala Lys Gly Ile Gln His Pro		
435	440	445
Pro Gln Ser Thr Ala Thr Val Ser Val Thr Val Ile Asp Val Asn Glu		
450	455	460
Asn Pro Tyr Phe Ala Pro Asn Pro Lys Ile Ile Arg Gln Glu Glu Gly		
465	470	475
Leu His Ala Gly Thr Val Leu Thr Thr Phe Thr Ala Gln Asp Pro Asp		
485	490	495
Arg Tyr Met Gln Gln Asn Ile Arg Tyr Thr Lys Leu Ser Asp Pro Ala		
500	505	510
Asn Trp Leu Lys Ile Asp Ser Val Asn Gly Gln Ile Thr Thr Ile Ala		
515	520	525
Val Leu Asp Arg Glu Ser Pro Asn Val Lys Ala Asn Ile Tyr Asn Ala		
530	535	540
Thr Phe Leu Ala Ser Asp Asn Gly Ile Pro Pro Met Ser Gly Thr Gly		
545	550	555
Thr Leu Gln Ile Tyr Leu Leu Asp Ile Asn Asp Asn Ala Pro Gln Val		
565	570	575
Leu Pro Gln Glu Ala Glu Ile Cys Glu Thr Pro Asp Pro Asn Ser Ile		
580	585	590
Asn Ile Thr Ala Leu Asp Tyr Asp Ile Asp Pro Asn Ala Gly Pro Phe		

595	600	605
Ala Phe Asp Leu Pro Leu Ser Pro Val Thr Ile Lys Arg Asn Trp Thr		
610	615	620
Ile Thr Arg Leu Asn Gly Asp Phe Ala Gln Leu Asn Leu Lys Ile Lys		
625	630	635 640
Phe Leu Glu Ala Gly Ile Tyr Glu Val Pro Ile Ile Ile Thr Asp Ser		
645	650	655
Gly Asn Pro Pro Lys Ser Asn Ile Ser Ile Leu Arg Val Lys Val Cys		
660	665	670
Gln Cys Asp Ser Asn Gly Asp Cys Thr Asp Val Asp Arg Ile Val Gly		
675	680	685
Ala Gly Leu Gly Thr Gly Ala Ile Ile Ala Ile Leu Leu Cys Ile Ile		
690	695	700
Ile Leu Leu Ile Leu Val Leu Met Phe Val Val Trp Met Lys Arg Arg		
705	710	715 720
Asp Lys Glu Arg Gln Ala Lys Gln Leu Leu Ile Asp Pro Glu Asp Asp		
725	730	735
Val Arg Asp Asn Ile Leu Lys Tyr Asp Glu Glu Gly Gly Gly Glu Glu		
740	745	750
Asp Gln Asp Tyr Asp Leu Ser Gln Leu Gln Gln Pro Asp Thr Val Glu		
755	760	765
Pro Asp Ala Ile Lys Pro Val Gly Ile Arg Arg Leu Asp Glu Arg Pro		
770	775	780
Ile His Ala Glu Pro Gln Tyr Pro Val Arg Ser Ala Ala Pro His Pro		
785	790	795 800
Gly Asp Ile Gly Asp Phe Ile Asn Glu Gly Leu Lys Ala Ala Asp Asn		
805	810	815
Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Leu Val Phe Asp Tyr Glu		
820	825	830
Gly Ser Gly Ser Thr Ala Gly Ser Leu Ser Ser Leu Asn Ser Ser Ser		
835	840	845
Ser Gly Gly Glu Gln Asp Tyr Asp Tyr Leu Asn Asp Trp Gly Pro Arg		

850

855

860

Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Asp Asp
 865 870 875

<210> 48

<211> 906

<212> PRT

<213> Mus musculus

<400> 48

Met Cys Arg Ile Ala Gly Gly Arg Gly Thr Leu Leu Pro Leu Leu Ala
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Ala Leu Leu Gln Ala Ser Val Glu Ala Ser Gly Glu Ile Ala Leu Cys
 20 25 30

Lys Thr Gly Phe Pro Glu Asp Val Tyr Ser Ala Val Leu Pro Lys Asp
 35 40 45

Val His Glu Gly Gln Pro Leu Leu Asn Val Lys Phe Ser Asn Cys Asn
 50 55 60

Arg Lys Arg Lys Val Gln Tyr Glu Ser Ser Glu Pro Ala Asp Phe Lys
 65 70 75 80

Val Asp Glu Asp Gly Thr Val Tyr Ala Val Arg Ser Phe Pro Leu Thr
 85 90 95

Ala Phe Gln Ala Lys Phe Leu Ile Tyr Ala Gln Asp Lys Glu Thr Gln
 100 105 110

Glu Lys Trp Gln Val Ala Val Asn Leu Ser Arg Glu Pro Thr Leu Thr
 115 120 125

Glu Glu Pro Met Lys Glu Pro His Glu Ile Glu Glu Ile Val Phe Pro
 130 135 140

Arg Gln Leu Ala Lys His Ser Gly Ala Leu Gln Arg Gln Lys Arg Asp
 145 150 155 160

Trp Val Ile Pro Pro Ile Asn Leu Pro Glu Asn Ser Arg Gly Pro Phe
 165 170 175

Pro Gln Glu Leu Val Arg Ile Arg Ser Asp Arg Asp Lys Asn Leu Ser
 180 185 190

Leu	Arg	Tyr	Ser	Val	Thr	Gly	Pro	Gly	Ala	Asp	Gln	Pro	Pro	Thr	Gly	195	200	205	
Ile	Phe	Ile	Ile	Asn	Pro	Ile	Ser	Gly	Gln	Leu	Ser	Val	Thr	Lys	Pro	210	215	220	
Leu	Asp	Arg	Glu	Leu	Ile	Ala	Arg	Phe	His	Leu	Arg	Ala	His	Ala	Val	225	230	235	240
Asp	Ile	Asn	Gly	Asn	Gln	Val	Glu	Asn	Pro	Ile	Asp	Ile	Val	Ile	Asn	245	250	255	
Val	Ile	Asp	Met	Asn	Asp	Asn	Arg	Pro	Glu	Phe	Leu	His	Gln	Val	Trp	260	265	270	
Asn	Gly	Ser	Val	Pro	Glu	Gly	Ser	Lys	Pro	Gly	Thr	Tyr	Val	Met	Thr	275	280	285	
Val	Thr	Ala	Ile	Asp	Ala	Asp	Asp	Pro	Asn	Ala	Leu	Asn	Gly	Met	Leu	290	295	300	
Arg	Tyr	Arg	Ile	Leu	Ser	Gln	Ala	Pro	Ser	Thr	Pro	Ser	Pro	Asn	Met	305	310	315	320
Phe	Thr	Ile	Asn	Asn	Glu	Thr	Gly	Asp	Ile	Ile	Thr	Val	Ala	Ala	Gly	325	330	335	
Leu	Asp	Arg	Glu	Lys	Val	Gln	Gln	Tyr	Thr	Leu	Ile	Ile	Gln	Ala	Thr	340	345	350	
Asp	Met	Glu	Gly	Asn	Pro	Thr	Tyr	Gly	Leu	Ser	Asn	Thr	Ala	Thr	Ala	355	360	365	
Val	Ile	Thr	Val	Thr	Asp	Trp	Asn	Asp	Asn	Pro	Pro	Glu	Glu	Thr	Ala	370	375	380	
Met	Thr	Phe	Tyr	Gly	Glu	Val	Pro	Glu	Asn	Arg	Val	Asp	Val	Ile	Val	385	390	395	400
Ala	Asn	Leu	Thr	Val	Thr	Asp	Lys	Asp	Gln	Pro	His	Thr	Pro	Ala	Trp	405	410	415	
Asn	Ala	Ala	Tyr	Arg	Ile	Ser	Gly	Gly	Asp	Pro	Thr	Gly	Arg	Phe	Ala	420	425	430	
Ile	Leu	Thr	Asp	Pro	Asn	Ser	Asn	Asp	Gly	Leu	Val	Thr	Val	Val	Lys	435	440	445	

Pro	Ile	Asp	Phe	Glu	Thr	Asn	Arg	Met	Phe	Val	Leu	Thr	Val	Ala	Ala		
450						455					460						
Glu	Asn	Gln	Val	Pro	Leu	Ala	Lys	Gly	Ile	Gln	His	Pro	Pro	Gln	Ser		
465					470					475					480		
Thr	Ala	Thr	Val	Ser	Val	Thr	Val	Ile	Asp	Val	Asn	Glu	Asn	Pro	Tyr		
				485					490					495			
Phe	Ala	Pro	Asn	Pro	Lys	Ile	Ile	Arg	Gln	Glu	Glu	Gly	Leu	His	Ala		
			500					505					510				
Gly	Thr	Met	Leu	Thr	Thr	Leu	Thr	Ala	Gln	Asp	Pro	Asp	Arg	Tyr	Met		
		515					520					525					
Gln	Gln	Asn	Ile	Arg	Tyr	Thr	Lys	Leu	Ser	Asp	Pro	Ala	Asn	Trp	Leu		
	530						535				540						
Lys	Ile	Asp	Pro	Val	Asn	Gly	Gln	Ile	Thr	Thr	Ile	Ala	Val	Leu	Asp		
545					550					555					560		
Arg	Glu	Ser	Pro	Tyr	Val	Gln	Asn	Asn	Ile	Tyr	Asn	Ala	Thr	Phe	Leu		
				565					570					575			
Ala	Ser	Asp	Asn	Gly	Ile	Pro	Pro	Met	Ser	Gly	Thr	Gly	Thr	Leu	Gln		
			580					585						590			
Ile	Tyr	Leu	Leu	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Gln	Val	Leu	Pro	Gln		
	595						600					605					
Glu	Ala	Glu	Thr	Cys	Glu	Thr	Pro	Glu	Pro	Asn	Ser	Ile	Asn	Ile	Ala		
	610					615					620						
Ala	Leu	Asp	Tyr	Asp	Ile	Asp	Pro	Asn	Ala	Gly	Pro	Phe	Ala	Phe	Asp		
625					630					635				640			
Leu	Pro	Leu	Ser	Pro	Val	Thr	Ile	Lys	Arg	Asn	Trp	Thr	Ile	Asn	Arg		
				645					650					655			
Leu	Asn	Gly	Asp	Phe	Ala	Gln	Leu	Asn	Leu	Lys	Ile	Lys	Phe	Leu	Glu		
		660						665					670				
Ala	Gly	Ile	Tyr	Glu	Val	Pro	Ile	Ile	Ile	Thr	Asp	Ser	Gly	Asn	Pro		
	675						680						685				
Pro	Lys	Ser	Asn	Ile	Ser	Ile	Leu	Arg	Val	Lys	Val	Cys	Gln	Cys	Asp		
	690					695						700					

Ser Asn Gly Asp Cys Thr Asp Val Asp Arg Ile Val Gly Ala Gly Leu
705 710 715 720

Gly Thr Gly Ala Ile Ile Ala Ile Leu Leu Cys Ile Ile Ile Leu Leu
725 730 735

Ile Leu Val Leu Met Phe Val Val Trp Met Lys Arg Arg Asp Lys Glu
740 745 750

Arg Gln Ala Lys Gln Leu Leu Ile Asp Pro Glu Asp Asp Val Arg Asp
755 760 765

Asn Ile Leu Lys Tyr Asp Glu Glu Gly Gly Gly Glu Glu Asp Gln Asp
770 775 780

Tyr Asp Leu Ser Gln Leu Gln Gln Pro Asp Thr Val Glu Pro Asp Ala
785 790 795 800

Ile Lys Pro Val Gly Ile Arg Arg Leu Asp Glu Arg Pro Ile His Ala
805 810 815

Glu Pro Gln Tyr Pro Val Arg Ser Ala Ala Pro His Pro Gly Asp Ile
820 825 830

Gly Asp Phe Ile Asn Glu Gly Leu Lys Ala Ala Asp Asn Asp Pro Thr
835 840 845

Ala Pro Pro Tyr Asp Ser Leu Leu Val Phe Asp Tyr Glu Gly Ser Gly
850 855 860

Ser Thr Ala Gly Ser Leu Ser Ser Leu Asn Ser Ser Ser Ser Gly Gly
865 870 875 880

Asp Gln Asp Tyr Asp Tyr Leu Asn Asp Trp Gly Pro Arg Phe Lys Lys
885 890 895

Leu Ala Asp Met Tyr Gly Gly Gly Asp Asp
900 905

<210> 49
<211> 912
<212> PRT
<213> Gallus gallus

<400> 49
Met Cys Arg Ile Ala Gly Thr Pro Pro Arg Ile Leu Pro Pro Leu Ala
1 5 10 15

Leu Met Leu Leu Ala Ala Leu Gln Gln Ala Pro Ile Lys Ala Thr Cys	20	25	30
Glu Asp Met Leu Cys Lys Met Gly Phe Pro Glu Asp Val His Ser Ala	35	40	45
Val Val Ser Arg Ser Val His Gly Gly Gln Pro Leu Leu Asn Val Arg	50	55	60
Phe Gln Ser Cys Asp Glu Asn Arg Lys Ile Tyr Phe Gly Ser Ser Glu	65	70	75
Pro Glu Asp Phe Arg Val Gly Glu Asp Gly Val Val Tyr Ala Glu Arg	85	90	95
Ser Phe Gln Leu Ser Ala Glu Pro Thr Glu Phe Val Val Ser Ala Arg	100	105	110
Asp Lys Glu Thr Gln Glu Glu Trp Gln Met Lys Val Lys Leu Thr Pro	115	120	125
Glu Pro Ala Phe Thr Gly Ala Ser Glu Lys Asp Gln Lys Lys Ile Glu	130	135	140
Asp Ile Ile Phe Pro Trp Gln Gln Tyr Lys Asp Ser Ser His Leu Lys	145	150	155
Arg Gln Lys Arg Asp Trp Val Ile Pro Pro Ile Asn Leu Pro Glu Asn	165	170	175
Ser Arg Gly Pro Phe Pro Gln Glu Leu Val Arg Ile Arg Ser Asp Arg	180	185	190
Asp Lys Ser Leu Ser Leu Arg Tyr Ser Val Thr Gly Pro Gly Ala Asp	195	200	205
Gln Pro Pro Thr Gly Ile Phe Ile Ile Asn Pro Ile Ser Gly Gln Leu	210	215	220
Ser Val Thr Lys Pro Leu Asp Arg Glu Gln Ile Ala Ser Phe His Leu	225	230	235
Arg Ala His Ala Val Asp Val Asn Gly Asn Gln Val Glu Asn Pro Ile	245	250	255
Asp Ile Val Ile Asn Val Ile Asp Met Asn Asp Asn Arg Pro Glu Phe	260	265	270

Pro Asp Arg Tyr Met Gln Gln Thr Ser Leu Arg Tyr Ser Lys Leu Ser
530 535 540

Asp Pro Ala Asn Trp Leu Lys Ile Asp Pro Val Asn Gly Gln Ile Thr
545 550 555 560

Thr Thr Ala Val Leu Asp Arg Glu Ser Ile Tyr Val Gln Asn Asn Met
565 570 575

Tyr Asn Ala Thr Phe Leu Ala Ser Asp Asn Gly Ile Pro Pro Met Ser
580 585 590

Gly Thr Gly Thr Leu Gln Ile Tyr Leu Leu Asp Ile Asn Asp Asn Ala
595 600 605

Pro Gln Val Asn Pro Lys Glu Ala Thr Thr Cys Glu Thr Leu Gln Pro
610 615 620

Asn Ala Ile Asn Ile Thr Ala Val Asp Pro Asp Ile Asp Pro Asn Ala
625 630 635 640

Gly Pro Phe Ala Phe Glu Leu Pro Asp Ser Pro Pro Ser Ile Lys Arg
645 650 655

Asn Trp Thr Ile Val Arg Ile Ser Gly Asp His Ala Gln Leu Ser Leu
660 665 670

Arg Ile Arg Phe Leu Glu Ala Gly Ile Tyr Asp Val Pro Ile Val Ile
675 680 685

Thr Asp Ser Gly Asn Pro His Ala Ser Ser Thr Ser Val Leu Lys Val
690 695 700

Lys Val Cys Gln Cys Asp Ile Asn Gly Asp Cys Thr Asp Val Asp Arg
705 710 715 720

Ile Val Gly Ala Gly Leu Gly Thr Gly Ala Ile Ile Ala Ile Leu Leu
725 730 735

Cys Ile Ile Ile Leu Leu Ile Leu Val Leu Met Phe Val Val Trp Met
740 745 750

Lys Arg Arg Asp Lys Glu Arg Gln Ala Lys Gln Leu Leu Ile Asp Pro
755 760 765

Glu Asp Asp Val Arg Asp Asn Ile Leu Lys Tyr Asp Glu Glu Gly Gly
770 775 780

Gly Glu Glu Asp Gln Asp Tyr Asp Leu Ser Gln Leu Gln Gln Pro Asp
785 790 795 800

Thr Val Glu Pro Asp Ala Ile Lys Pro Val Gly Ile Arg Arg Leu Asp
805 810 815

Glu Arg Pro Ile His Ala Glu Pro Gln Tyr Pro Val Arg Ser Ala Ala
820 825 830

Pro His Pro Gly Asp Ile Gly Asp Phe Ile Asn Glu Gly Leu Lys Ala
835 840 845

Ala Asp Asn Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Leu Val Phe
850 855 860

Asp Tyr Glu Gly Ser Gly Ser Thr Ala Gly Ser Leu Ser Ser Leu Asn
865 870 875 880

Ser Ser Ser Ser Gly Gly Glu Gln Asp Tyr Asp Tyr Leu Asn Asp Trp
885 890 895

Gly Pro Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Asp Asp
900 905 910

<210> 50
<211> 129
<212> DNA
<213> Homo sapiens

<400> 50
atgaagctcc ttttgctgac tttgactgtg ctgctgctct tatcccagct gactccaggt 60
ggcaccctaaa gatgctggaa tctttatggc aaatgccgtt acagatgctc caagaaggaa 120
agagtctat 129

<210> 51
<211> 117
<212> DNA
<213> Homo sapiens

<400> 51

aaggcacact gtaaatacaa gttgagtaac cctaataaaa aaatctgaaa tctaaaatgc 60
tccaaaatcc aaaacttttt gagtgccaac atgatgctca aaggaaatgc tcattgg 117

<210> 52
<211> 89
<212> DNA
<213> Homo sapiens

<400> 52
gagtgagact ccgtctcaaa aaaacaaaaa caaaaacaaa aacaaaaaca aaaacaagaa 60
atgcatccat attaacttcc aaatgcaaa 89

<210> 53
<211> 86
<212> DNA
<213> Homo sapiens

<400> 53
ggcactatct tactttgagg tgattacatt gctttactca aagaacttgg tggaatggct 60
aaagttttta aaacaaacaa aactaa 86

<210> 54
<211> 29
<212> DNA
<213> Homo sapiens

<400> 54
caaaaataaa acaaaacaaa agaataaag 29

<210> 55
<211> 854
<212> DNA
<213> Homo sapiens

<400> 55
atgaagcggc agaacgtgcg cacgctggcg ctcatcgtgt gcaccttcac ctacctgctg 60
gtgggcgccc cggtcttcga cgcgctggag tcggagcccg agctgatcga ggggcagcgg 120
ctggagctgc ggcagcagga gctgcgggcg cgctacaacc tcagccaggg cggctacgag 180

gagctggagc gcgctgtgct ggcctcaag ccgcacaagg ccggcgtgca gtggcgcttc 240
gccggctcct tctacttcgc catcacgctc atcaccacca tcggctacgg gcacgcggca 300
cccagcacgg atggcgggcaa ggtgttctgc atgttctacg cgctgctggg catcccgtc 360
acgctcgtca tgttccagag cctgggcgag cgcacaaaca ccttggtgag gtacctgctg 420
caccgcgcca agaaggggct gggcatgcgg cgcgccgacg tgtccatggc caacatggtg 480
ctcatcggtt ttttctcgtg catcagcacg ctgtgcatcg gcgcgcgcgc cttctccac 540
tacgagcact ggaccttctt ccaggcctac tactactgct tcatcaccct caccaccatc 600
ggcttcggcg actacgtggc gctgcagaag gaccaggccc tgcagacgca gccgcagtac 660
gtggccttca gcttcgtcta catccttacg ggccctcacg tcatcggcgc cttcctcaac 720
ctcgtggtgc tgcgcttcat gaccatgaac gccgaggacg agaagcgcca cgccgagcac 780
cgcgcgctgc tcacgcgcaa cgggcaggcg ggcggcggcg gaggggggtgg cagcgcgcac 840
actacggaca ccgc 854

<210> 56
<211> 1286
<212> DNA
<213> Homo sapiens

<400> 56
ggagcgcgcg gtccgggcac acggagcagg ttgggaccgc ggcgggtacc ggggcccggg 60
cgccatgcgg aggcgagcg tgcgcgcggc cgggctggtc ctgtgcaccc tgtgttacct 120
gctggtgggc gctgctgtct tcgacgcgct cgagtcgag gcggaaagcg gccgccagcg 180
actgctggtc cagaagcggg gcgctctccg gaggaagttc ggcttctcgg ccgaggacta 240
ccgcgagctg gagcgcttg cgctccaggc tgagccccac cgcgccggcc gccagtggaa 300
gttccccggc tccttctact tcgccatcac cgtcatcact accatcgggt acggccacgc 360
cgcgcgggt acggactccg gcaaggctt ctgcatgttc tacgcgctcc tgggcatccc 420
gctgacgctg gtcactttcc agagcctggg cgaacggctg aacgcggtgg tgcggcgcc 480
cctgttggcg gccaaagtgt gcctgggcct gcggtggacg tgcgtgtcca cggagaacct 540

ggtggtggcc gggctgctgg cgtgtgccgc caccctggcc ctcggggccc tgcctttctc 600
 gcacttcgag ggctggacct tcttcacgc ctactactac tgcttcatca cctcaccac 660
 catcggcttc ggcgacttcg tggcactgca gagcggcgag gcgctgcaga ggaagctccc 720
 ctacgtggcc ttcagcttcc tctacatcct cctgggggctc acggtcattg gcgccttcct 780
 caacctggtg gtcttgcgct tctcgttgc cagcgcgcac tggcccgcgc gcgctgccc 840
 cccccccagc ccgcgcccc cggggggcgcc cgagagccgt ggctcttggc tgccccgcgc 900
 cccggcccgc tccgtgggct ccgcctctgt cttctgccac gtgcacaagc tggagaggtg 960
 cgcccgcgc aacctgggct ttctgcccc ctcgagccc ggggtcgtgc gtggcgggca 1020
 ggctcccagg cctggggccc ggtggaagtc catctgacaa cccacccag gccagggtcg 1080
 aatctggaat gggagggtct ggcttcagct atcagggcac cctccccagg gattggaac 1140
 ggatgacggg cctctaggcg gtcttctgca cgagcaagtt tctcattact gtctgtggct 1200
 aagtcccctc ccttctttcc aaaaatatat tacagtcacc ccataaaaaa aaaaaaaaaa 1260
 aaaaaaaaaa aaaaaaaaaa aaaaaa 1286

<210> 57
 <211> 1286
 <212> DNA
 <213> Homo sapiens

<400> 57
 ggagcgcgcg gtccgggcac acggagcagg ttgggaccgc ggcgggtacc ggggccgggg 60
 cgccatgcgg aggccgagcg tgcgcgcggc cgggctggct ctgtgcaccc tgtgttacct 120
 gctggtgggc gctgctgtct tcgacgcgct cgagtcagag gcgaaaagcg gccgccagcg 180
 actgctggtc cagaagcggg gcgctctccg gaggaagttc ggcttctcgg ccgaggacta 240
 ccgcgagctg gagcgcttgg cgctccagge tgagccccac cgcgcgggccc gccagtggaa 300
 gttccccggc tctttctact tcgccatcac cgtcatcact accatcgggt acggccacgc 360
 cgcgcggggt acggactccg gcaaggcttt ctgcatgttc tacgcgctcc tgggcatccc 420

gctgacgctg gtcactttcc agagcctggg cgaacggctg aacgcggtgg tgcggcgcct 480
cctggtggcg gccaaagtgt gcctgggcct gcggtggacg tgcgtgtcca cggagaacct 540
ggtggtggcc gggctgctgg cgtgtgccgc caccctggcc ctcgggggccg tcgccttctc 600
gcacttcgag ggctggacct tcttcacgc ctactactac tgcttcatca ccctcaccac 660
catcggcttc ggcgacttcg tggcactgca gagcggcgag gcgctgcaga ggaagctccc 720
ctacgtggcc ttcagcttcc tctacatcct cctggggctc acggtcattg gcgccttcct 780
caacctggtg gtctgctgt tctcgttgc cagcgcgcagc tggcccgagc gcgctgcccg 840
ccccccagc ccgcgcccc cggggggcgc cgagagccgt ggctcttggc tgccccgccc 900
cccggccgc tccgtgggtt ccgcctctgt cttctgccac gtgcacaagc tggagaggtg 960
cgcccgcgac aacctgggtt tttcgcccc ctcgagcccg ggggtcgtgc gtggcgggca 1020
ggctcccagg cctggggccc ggtggaagtc catctgacaa cccacccag gccaggggtcg 1080
aatctggaat gggaggggtt ggcttcagct atcagggcac cctccccagg gattggaaac 1140
ggatgacggg cctctaggcg gtcttctgca cgagcaagtt tctcattact gtctgtggct 1200
aagtccccct ctttctttcc aaaaatatat tacagtcacc ccataaaaaa aaaaaaaaaa 1260
aaaaaaaaa aaaaaaaaaa aaaaaa 1286

<210> 58
<211> 330
<212> PRT
<213> Homo sapiens

<400> 58
Met Arg Arg Pro Ser Val Arg Ala Ala Gly Leu Val Leu Cys Thr Leu
1 5 10 15
Cys Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu
20 25 30
Ala Glu Ser Gly Arg Gln Arg Leu Leu Val Gln Lys Arg Gly Ala Leu
35 40 45
Arg Arg Lys Phe Gly Phe Ser Ala Glu Asp Tyr Arg Glu Leu Glu Arg
50 55 60

Leu Ala Leu Gln Ala Glu Pro His Arg Ala Gly Arg Gln Trp Lys Phe
 65 70 75 80
 Pro Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Glu Tyr
 85 90 95
 Gly His Ala Ala Pro Gly Thr Asp Ser Gly Lys Val Phe Cys Met Phe
 100 105 110
 Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Phe Gln Ser Leu
 115 120 125
 Gly Glu Arg Leu Asn Ala Val Val Arg Arg Leu Leu Leu Ala Ala Lys
 130 135 140
 Cys Cys Leu Gly Leu Arg Trp Thr Cys Val Ser Thr Glu Asn Leu Val
 145 150 155 160
 Val Ala Gly Leu Leu Ala Cys Ala Ala Thr Leu Ala Leu Gly Ala Val
 165 170 175
 Ala Phe Ser His Phe Glu Gly Trp Thr Phe Phe His Ala Tyr Tyr Tyr
 180 185 190
 Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Phe Val Ala Leu
 195 200 205
 Gln Ser Gly Glu Ala Leu Gln Arg Lys Leu Pro Tyr Val Ala Phe Ser
 210 215 220
 Phe Leu Tyr Ile Leu Leu Gly Leu Thr Val Ile Gly Ala Phe Leu Asn
 225 230 235 240
 Leu Val Val Leu Arg Phe Leu Val Ala Ser Ala Asp Trp Pro Glu Arg
 245 250 255
 Ala Ala Arg Thr Pro Ser Pro Arg Pro Pro Gly Ala Pro Glu Ser Arg
 260 265 270
 Gly Leu Trp Leu Pro Arg Arg Pro Ala Arg Ser Val Gly Ser Ala Ser
 275 280 285
 Val Phe Cys His Val His Lys Leu Glu Arg Cys Ala Arg Asp Asn Leu
 290 300
 Gly Phe Ser Pro Pro Ser Ser Pro Gly Val Val Arg Gly Gly Gln Ala
 305 310 315 320

Pro Arg Leu Gly Ala Arg Trp Lys Ser Ile
 325 330

<210> 59

<211> 330

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Arg Pro Ser Val Arg Ala Ala Gly Leu Val Leu Cys Thr Leu
 1 5 10 15

Cys Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu
 20 25 30

Ala Glu Ser Gly Arg Gln Arg Leu Leu Val Gln Lys Arg Gly Ala Leu
 35 40 45

Arg Arg Lys Phe Gly Phe Ser Ala Glu Asp Tyr Arg Glu Leu Glu Arg
 50 55 60

Leu Ala Leu Gln Ala Glu Pro His Arg Ala Gly Arg Gln Trp Lys Phe
 65 70 75 80

Pro Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr
 85 90 95

Gly His Ala Ala Pro Gly Thr Asp Ser Gly Lys Val Phe Cys Met Phe
 100 105 110

Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Phe Gln Ser Leu
 115 120 125

Gly Glu Arg Leu Asn Ala Val Val Arg Arg Leu Leu Leu Ala Ala Lys
 130 135 140

Cys Cys Leu Gly Leu Arg Trp Thr Cys Val Ser Thr Glu Asn Leu Val
 145 150 155 160

Val Ala Gly Leu Leu Ala Cys Ala Ala Thr Leu Ala Leu Gly Ala Val
 165 170 175

Ala Phe Ser His Phe Glu Gly Trp Thr Phe Phe His Ala Tyr Tyr Tyr
 180 185 190

Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Phe Val Ala Leu

195	200	205
Gln Ser Gly Glu Ala Leu	Gln Arg Lys Leu Pro Tyr Val Ala Phe Ser	
210	215	220
Phe Leu Tyr Ile Leu Leu Gly Leu Thr Val Ile Gly Ala Phe Leu Asn		
225	230	235 240
Leu Val Val Leu Arg Phe Leu Val Ala Ser Ala Asp Trp Pro Glu Arg		
245	250	255
Ala Ala Arg Pro Pro Ser Pro Arg Pro Pro Gly Ala Pro Glu Ser Arg		
260	265	270
Gly Leu Trp Leu Pro Arg Arg Pro Ala Arg Ser Val Gly Ser Ala Ser		
275	280	285
Val Phe Cys His Val His Lys Leu Glu Arg Cys Ala Arg Asp Asn Leu		
290	295	300
Gly Phe Ser Pro Pro Ser Ser Pro Gly Val Val Arg Gly Gly Gln Ala		
305	310	315 320
Pro Arg Pro Gly Ala Arg Trp Lys Ser Ile		
325	330	
<210> 60		
<211> 365		
<212> PRT		
<213> Cavia porcellus		
<400> 60		
Met Lys Lys Gln Asn Val Arg Thr Leu Ser Leu Ile Ala Cys Thr Phe		
1	5	10 15
Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Asp		
20	25	30
His Glu Met Arg Glu Glu Glu Lys Leu Lys Ala Glu Glu Ile Arg Ile		
35	40	45
Arg Gly Lys Tyr Asn Ile Ser Thr Glu Asp Tyr Arg Gln Leu Glu Leu		
50	55	60
Val Ile Leu Gln Ser Glu Pro His Arg Ala Gly Val Gln Trp Lys Phe		
65	70	75 80

Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr	85	90	95
Gly His Ala Ala Pro Gly Thr Asp Ala Gly Lys Ala Phe Cys Met Phe	100	105	110
Tyr Ala Val Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu	115	120	125
Gly Glu Arg Met Asn Thr Phe Val Arg Tyr Leu Leu Lys Arg Ile Lys	130	135	140
Lys Cys Cys Gly Met Arg Asn Thr Glu Val Ser Met Glu Asn Met Val	145	150	155
Thr Val Gly Phe Phe Ser Cys Met Gly Thr Leu Cys Ile Gly Ala Ala	165	170	175
Ala Phe Ser Gln Cys Glu Glu Trp Ser Phe Phe His Ala Tyr Tyr Tyr	180	185	190
Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu	195	200	205
Gln Ser Lys Gly Ala Leu Gln Arg Lys Pro Phe Tyr Val Ala Phe Ser	210	215	220
Phe Met Tyr Ile Leu Val Gly Leu Thr Val Ile Gly Ala Phe Leu Asn	225	230	235
Leu Val Val Leu Arg Phe Leu Thr Met Asn Ser Asp Glu Glu Arg Gly	245	250	255
Glu Gly Glu Glu Gly Ala Ala Leu Pro Gly Asn Pro Ser Ser Val Val	260	265	270
Thr His Ile Ser Glu Glu Ala Arg Gln Val Arg Gln Arg Tyr Arg Gly	275	280	285
Glu Gly Gly Asp Leu Gln Ser Val Cys Ser Cys Ala Cys Tyr Arg Ser	290	295	300
Gln Pro Gln Asn Phe Gly Ala Thr Leu Ala Pro Gln Pro Leu His Ser	305	310	315
Ile Ser Cys Arg Ile Glu Glu Ile Ser Pro Ser Thr Leu Lys Asn Ser	325	330	335

Leu Phe Pro Ser Pro Ile Ser Ser Val Ser Pro Gly Leu His Ser Phe
 340 345 350

Gly Asp Asn His Arg Leu Met Leu Arg Arg Lys Ser Val
 355 360 365

<210> 61

<211> 258

<212> PRT

<213> Mus musculus

<400> 61

Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr Phe
 1 5 10 15

Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu
 20 25 30

Pro Glu Met Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Leu Glu Leu
 35 40 45

Arg Ala Arg Tyr Asn Leu Ser Glu Gly Gly Tyr Glu Glu Leu Glu Arg
 50 55 60

Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe
 65 70 75 80

Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr
 85 90 95

Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe
 100 105 110

Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu
 115 120 125

Gly Glu Arg Ile Asn Thr Phe Val Arg Tyr Leu Leu His Arg Ala Lys
 130 135 140

Arg Gly Leu Gly Met Arg His Ala Glu Val Ser Met Ala Asn Met Val
 145 150 155 160

Leu Ile Gly Phe Val Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala
 165 170 175

Ala Phe Ser Tyr Tyr Glu Arg Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr
 180 185 190

Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu
 195 200 205

Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser
 210 215 220

Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn
 225 230 235 240

Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg
 245 250 255

Asp Ala

<210> 62

<211> 35

<212> PRT

<213> Mus musculus

<400> 62

Ser Cys Leu Ser Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro
 1 5 10 15

Val Thr Cys Ala Ala Ala Ala Gly Gly Val Gly Val Gly Val Gly Gly
 20 25 30

Ser Gly Phe
 35

<210> 63

<211> 39

<212> PRT

<213> Mus musculus

<400> 63

Thr Cys Val Glu His Ser His Ser Ser Pro Gly Gly Gly Gly Arg Tyr
 1 5 10 15

Ser Asp Thr Pro Ser His Pro Cys Leu Cys Ser Gly Thr Gln Arg Ser
 20 25 30

Ala Ile Ser Ser Val Ser Thr
 35

<210> 64
<211> 388
<212> DNA
<213> Homo sapiens

<400> 64
aggcggcatc tgctggctct gctgctgctc ctctctaccc tggatgaccc ctccgctgca 60
gctcctatcc atgatgctga cgcccaagag agctccttgg gtctcacagg cctccagagc 120
ctactccaag gcttcagccg acttttctctg aaaggtaacc tgcttcgggg catagacagc 180
ttattctctg ccccatgga cttccggggc ctccctggga actaccacaa agaggagaac 240
caggagcacc agctggggaa caacaccctc tccagccacc tccagatoga caagatgacc 300
gacaacaaga caggagaggt gctgatctcc gagaatgtgg tggcatccat tcaaccagcg 360
gaggggagct tcgaggggtga tttgaagg 388

<210> 65
<211> 322
<212> DNA
<213> Homo sapiens

<400> 65
ggagaaggag gccctggtac ccatccagaa ggccacggac agcttccaca cagaactcca 60
tccccgggtg gccttctgga tcattaagct gccacggcgg aggtcccacc aggatgccct 120
ggagggcggc cactggetca gcgagaagcg acaccgctg caggccatcc gggatggact 180
ccgcaagggg acccacaagg acgtcctaga agaggggacc gagagctcct ccactccag 240
gctgtcccc cgaaagaccc acttactgta catcctcagg ccctctcggc agctgtaggg 300
gtggggaccg gggagcacct gc 322

<210> 66
<211> 218
<212> PRT
<213> Homo sapiens

<400> 66
Arg His Leu Leu Val Leu Leu Leu Leu Ser Thr Leu Val Ile Pro

1	5	10	15
Ser Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu			
20	25	30	
Gly Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe			
35	40	45	
Leu Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro			
50	55	60	
Met Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln			
65	70	75	80
Glu His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp			
85	90	95	
Lys Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val			
100	105	110	
Val Ala Ser Ile Gln Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys			
115	120	125	
Val Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala			
130	135	140	
Thr Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile			
145	150	155	160
Ile Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly			
165	170	175	
His Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly			
180	185	190	
Leu Arg Lys Gly Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser			
195	200	205	
Ser Ser His Ser Arg Leu Ser Pro Arg Lys			
210	215		

<210> 67

<211> 15

<212> PRT

<213> Homo sapiens

<400> 67

Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg Gln Leu
 1 5 10 15

<210> 68

<211> 242

<212> PRT

<213> Homo sapiens

<400> 68

Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 1 5 10 15

Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
 20 25 30

Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 35 40 45

Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 50 55 60

Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 65 70 75 80

Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
 85 90 95

Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
 100 105 110

Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
 115 120 125

Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
 130 135 140

Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
 145 150 155 160

Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
 165 170 175

Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
 180 185 190

Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
 195 200 205

His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
 210 215 220

Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
 225 230 235 240

Gln Leu

<210> 69

<211> 230

<212> PRT

<213> Mus musculus

<400> 69

Met Cys Arg Leu Arg Val Leu Leu Leu Leu Leu Pro Leu Ala Phe Val
 1 5 10 15

Ser Ser Ser Ala Leu Pro Ile His Asp Val Asp Ser Gln Gln Asn Thr
 20 25 30

Ser Gly Phe Leu Gly Leu Gln Arg Leu Leu Gln Ser Phe Ser Arg Leu
 35 40 45

Phe Leu Lys Asn Asp Leu Leu Arg Asp Leu Asp Asn Phe Phe Ser Ser
 50 55 60

Pro Met Asp Phe Arg Asp Leu Pro Arg Asn Phe His Gln Glu Glu Asn
 65 70 75 80

Gln Glu His Arg Met Gly Asn His Thr Leu Ser Ser His Leu Gln Ile
 85 90 95

Asp Lys Val Thr Asp Asn Gln Thr Gly Glu Val Leu Ile Ser Glu Lys
 100 105 110

Val Glu Ala Ser Ile Glu Pro Glu Arg Asn Pro Glu Gly Asp Trp Lys
 115 120 125

Val Pro Lys Val Glu Ala Lys Glu Pro Pro Val Pro Val Gln Lys Val
 130 135 140

Thr Asp Ser Leu His Pro Glu Pro Arg Gln Val Ala Phe Trp Ile Met
 145 150 155 160

Lys Met Pro Arg Arg Arg Thr Gln Pro Asp Val Gln Asp Gly Gly Arg

Leu Val Thr Gly Glu Phe Leu Glu Leu Asp Leu Asn Thr Leu Val Gly			
225	230	235	240
Glu Ala Gly Gly Asp Leu Ile Asp Tyr Pro Leu Gly Arg Pro Ala Met			
	245	250	255
Leu Pro Arg Pro Gln Met Pro Glu Leu Pro Pro Met Gly Asp Asn Thr			
	260	265	270
Asn Ser Gln Leu Ala Ile Ser Ala Asn Phe Leu Ser Ser Val Leu Thr			
	275	280	285
Met Leu Gln Lys Gln Gly Ala Leu Asp Ile Asp Ile Thr Asp Gly Met			
	290	295	300
Phe Glu Asp Leu Pro Pro Leu Thr Thr Ser Thr Leu Gly Ala Leu Ile			
305	310	315	320
Pro Lys Val Phe Gln Gln Tyr Pro Glu Ser Arg Pro Leu Thr Ile Arg			
	325	330	335
Ile Gln Val Pro Asn Pro Pro Thr Val Thr Leu Gln Lys Asp Lys Ala			
	340	345	350
Leu Val Lys Val Phe Ala Thr Ser Glu Val Val Val Ser Gln Pro Asn			
	355	360	365
Asp Val Glu Thr Thr Ile Cys Leu Ile Asp Val Asp Thr Asp Leu Leu			
	370	375	380
Ala Ser Phe Ser Val Glu Gly Asp Lys Leu Met Ile Asp Ala Lys Leu			
385	390	395	400
Asp Lys Thr Ser Leu Asn Leu Arg Thr Ser Asn Val Gly Asn Phe Asp			
	405	410	415
Val Phe Ile Leu Glu Met Leu Val Glu Lys Ile Phe Asp Leu Ala Phe			
	420	425	430
Met Pro Ala Met Asn Ala Ile Leu Gly Ser Gly Val Pro Leu Pro Lys			
	435	440	445
Ile Leu Asn Ile Asp Phe Ser Asn Ala Asp Ile Asp Val Leu Glu Asp			
	450	455	460
Leu Leu Val Leu Ser Thr			
465	470		

<210> 72
 <211> 473
 <212> PRT
 <213> Rattus norvegicus

<400> 72

Met Met Pro Gly Val Tyr Ala Leu Leu Leu Leu Trp Gly Leu Ala Thr
 1 5 10 15

Pro Cys Leu Gly Leu Leu Glu Thr Val Gly Thr Leu Ala Arg Ile Asp
 20 25 30

Lys Asp Glu Leu Gly Lys Ala Ile Gln Asn Ser Leu Val Gly Gly Pro
 35 40 45

Ile Leu Gln Asn Val Leu Gly Thr Val Thr Ser Val Asn Gln Gly Leu
 50 55 60

Leu Gly Ala Gly Gly Leu Leu Gly Gly Gly Gly Leu Leu Ser Tyr Gly
 65 70 75 80

Gly Leu Phe Ser Leu Val Glu Glu Leu Ser Gly Leu Lys Ile Glu Glu
 85 90 95

Leu Thr Leu Pro Thr Val Ser Ile Lys Leu Leu Pro Gly Val Gly Val
 100 105 110

Gln Leu Ser Leu His Thr Lys Val Ser Leu His Gly Ser Gly Pro Leu
 115 120 125

Val Gly Leu Leu Gln Leu Ala Ala Glu Val Asn Val Ser Ser Lys Val
 130 135 140

Ala Leu Gly Met Ser Pro Arg Gly Thr Pro Ile Leu Ile Leu Lys Arg
 145 150 155 160

Cys Asn Thr Leu Leu Gly His Ile Ser Leu Thr Ser Gly Leu Leu Pro
 165 170 175

Thr Pro Ile Phe Gly Leu Val Glu Gln Thr Leu Cys Lys Val Leu Pro
 180 185 190

Gly Leu Leu Cys Pro Val Val Asp Ser Val Leu Ser Val Val Asn Glu
 195 200 205

Leu Leu Gly Ala Thr Leu Ser Leu Val Pro Leu Gly Pro Leu Gly Ser

210	215	220
Val Glu Phe Thr Leu Ala Thr Leu Pro Leu Ile Ser Asn Gln Tyr Ile		
225	230	235 240
Glu Leu Asp Ile Asn Pro Ile Val Lys Ser Ile Ala Gly Asp Val Ile		
245	250	255
Asp Phe Pro Lys Pro Arg Leu Pro Val Lys Met Pro Pro Lys Glu Asp		
260	265	270
His Thr Ser Gln Val Thr Val Pro Leu Tyr Leu Phe Asn Thr Val Phe		
275	280	285
Gly Leu Leu Gln Thr Asn Gly Ala Leu Asp Leu Asp Ile Thr Pro Glu		
290	295	300
Met Val Pro Arg Asn Ile Pro Leu Thr Thr Thr Asp Leu Ala Ala Leu		
305	310	315 320
Ala Pro Glu Ala Leu Gly Lys Leu Pro Pro Gly Gln His Leu Leu Leu		
325	330	335
Ser Leu Arg Val Met Lys Ser Pro Met Ile Leu Leu Gln Asn Lys Lys		
340	345	350
Val Thr Val Ser Ile Pro Val Thr Ile His Val Leu Ser Ser Val Pro		
355	360	365
Gln Gly Thr Pro Val Ala Leu Phe Gln Met Asn Gly Val Met Thr Leu		
370	375	380
Asn Ala His Leu Val Pro Ser Thr Thr Lys Leu His Ile Ser Leu Ser		
385	390	395 400
Leu Glu Arg Leu Thr Val Gln Leu Ala Ser Ser Phe Ser Gln Pro Phe		
405	410	415
Asp Ala Ser Arg Leu Glu Glu Trp Leu Ser Asp Val Val Arg Ala Ala		
420	425	430
Tyr Met Gln Lys Leu Asn Glu His Leu Glu Val Gly Ile Pro Leu Pro		
435	440	445
Lys Ile Leu Asn Val Asn Phe Ala Asn Ser Val Val Asp Val Ile Glu		
450	455	460
Asn Ala Val Val Leu Thr Val Ala Pro		

465

470

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